Human prostate tum Prostate tumour pr Human mast cell re

ABG94411 ABG76665

Human L1-12 protei Human PROST 03. H breast tumou Prostate tumour an

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ABB77575
ABG61900
ABB95222
AAU10324
AAU82643
ABU71653
AAB74830
AAB771860
AAM501318

Prostate specific Prostate cancer

Thioredoxin-ubiqui Alpha prepro-P501S Human prostate spe Thioredoxin-ubiqui Human prostate CDN P553S splice varia Human P553S splice Prostate cancer as Human albumin fusi Human albumin fusi Human prostate pro Ral2-P501S-E2 cons Ral2-P501S-E2 cons

AAM50662 AAU69875 AAM01230 ABB95335

AAE01362 ABG64105 AAU69907 AAM01262

ABU71766

ABU71798 AAW85068

371 400 400 400 400 255 255 255 255 255

Minimum DB Maximum DB

Database

Searched:

AAB29268

ABB95367

AAU04205 AAO19084 AAY54369 AAE01423 ABB77571 ABB60709 AAM40227

OM protein

Run on:

Sequence:

Title: Perfect

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Prostate; cancer; tumour; vaccine; immunogen; clone
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97US-0806099.
97US-0904804.
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N-PSDB; AAV61201.
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Prostate tumour sp
Protein encoded by
Human immunogenic
Human prostate cDN
Human prostate tum
                                                                                                      (without alignments)
1867.570 Million cell updates/sec
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| SIDSI/gcgdata/geneseqp-embl/AA1981.DAT:*
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                                                                                      December 3, 2003, 17:15:11 ; Search time 47 Seconds
            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Human mast cell re Drosophila melanog Human polypeptide Human prostate cDN P553S splice varia

ALIGNMENTS

AAM01228

prostate proteins

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Polypeptides comprising immunogenic portions

Human prostate-spe Human prostate-spe Human P501S invent

100.0 100.0 100.0

450780

Result 8

98WO-US03492.

Prostate-specific Human prostate-spe Amino acid sequenc Human secreted pro

Prostate cancer as Protein encoded by Human prostate-rel

97US-0806596. 97US-0904809. 98US-0020747.

CORP.

<u>د.</u>

98WO-US03690

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This sequence is encoded by a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as this protein sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
                                                                                                                                                                                                                                                           Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers
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01-AUG-1997;
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                                          The present sequence is an immunogenic portion of a prostate tumour protein. The immunogen, or the DNA encoding it, can be used as a vaccine for the treatment of prostate cancer. The immunogen was isolated from a prostate tumour cDNA library obtained by subtracting a prostate tumour cDNA library with a normal tissue cDNA library.
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                    Length 553;
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                    DB 19;
                      Score 2861; DB 19;
Pred. No. | 2.2e-269;
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100.0%; Scor.
100.0%; Pred. No. z..
0; Mismatches
                Query Match
Best Local Similarity 100.
Matches 553; Conservative
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specific gene; human; prostate cancer; detection;

Prostate tumour

therapy.

Prostate

Homo sapiens

tumour specific gene clone L1-12 protein.

(updated)
(first entry)

25-MAR-2003 08-DEC-1998

AAW69385

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AAW69385 standard; Protein; 553

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241 CCPCRARLAFRNLGALLPRLHOLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGEGL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; diagnosis; tumour; gene therapy; detection;
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14-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is encoded by a cDNA sequence which was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immunotherapy and diagnosis of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to produce a vaccine.
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Best Local Similarity 100.
Marches 553; Conservative
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the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polymucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06241 to AAA06691 and AAY82000 to AAY82020 represent sequences used in the exemplification of
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The invention relates to isolated prostate-specific polynuclectides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides or antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
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                                                                                                                                                                                                                                                                                                                                                                                         New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVQRLMVSRLLRHRKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PVLGLVCVPLLGSASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDPRPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CCPCRARLAFRNIGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGEGL
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                                                                                                                                                                                                                                                                         Kalos MD;
Carter D;
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A, Day CH, Vedvick TS,
epler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2861; DB 22;
Pred. No. 2.2e-269;
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GR, Retter MW, Stolk JA, Day G
Wang A, Skeiky YAW, Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 269-270; 579pp; English.
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                                                                                                                                                                   2000US-0657279.
2000US-0679426.
2000US-0685166.
                                                                2000US-0568100
2000US-0570737
                                                                                                   2000US-0593793
                                                                                                                     000US-0605783
                                                                                                                                   2000US-0636215
                                                                                                                                                   2000US-0651236
              2001WO-US09919
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Best Local Similarity 100.
Matches 553; Conservative
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                                                                                                 13-JUN-2000;
27-JUN-2000;
                                                                                                                                                                       06-SEP-2000;
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                                                                09-MAY-2000;
12-MAY-2000;
                                                                                                                                   10-AUG-2000;
                27-MAR-2001;
                                                                                                                                                     29-AUG-2000;
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                                                                                                                                                                                                                                                                                          Fanger
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   ELALLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCRQAYSVYAFMISLGGCLGYLLPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes polynucleotide sequences (I) which encod prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene | therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient.
                                                                                            241 CCPCRARLAFRNLGALLPRIHQLCCRMPRILRRLFVAELCSWMALMTFTLFYTDFVGEGL
                                          421 ASSEDSIMITSFLPGPKPGAPFPNGHVGAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA
                                                                                                                                                                                                                                                                                                   481 RVVPGKGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ
                                                                                                                                YQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA
                                                                                                                                                                                AFPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG
                                                                                                                                                                                                                                 ASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPPALCGASACDVSVRVVVGEPTEA
                                                                                                                                                                                                                                                                                     RVVPGRGICLDLAILDSAFILSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SL, |Jiang Y, Reed SG;
Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate-specific amino acid sequence Ll<sub>†</sub>12.
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Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 267-268; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             AAM01117 standard; Protein; 553 AA.
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GR, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-2001; 2001WO-US01574.
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                                                                                                                                                                                                                                                                                                                                                      VVFDKSDLAKYSA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Kalos MD, Fanger GR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is a partial prostate tumour protein, encoded by a prostate tumour specific cDNA. The DNA is useful for inhibiting the development of prostate cancer or for treating prostate cancer in a patient.
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                                                                                       RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ
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                                      ASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotide encoding polypeptide comprising a portion of prostate tumour protein useful for inhibiting development of prostate cancer or for treating prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVQRLWVSRLLRHRKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIG
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                                                                                                                                                                                                                                                                                                                                     Human; prostate tumour protein; prostate cancer
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                                                                                                                                                                                                                                                                                                           Human prostate tumour protein L1-12
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                                                                                                                                                                                                                                AAU04961 standard; Protein; 553
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97US-0904804.
98US-0020956.
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                                                                                                                                       VVFDKSDLAKYSA 553
                                                                                                                                                                VVPDKSDLAKYSA 553
                                                                                                                                                                                                                                                                                  (first entry)
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Matches 553; Conservative
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N-PSDB; AAS10108.
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                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                      421
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18-NOV-1999;
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(I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies of (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polymucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                  IDWDTSALAPYLGTQEECLFGLTLIFLIFLTCVAATLLVAEBAALGPTEPAEGLSAPSLSPH
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                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                 Match 100.0%; Score 2861; DB 22; Length 553; Local Similarity 100.0%; Pred. No. 2.2e-269; les 553; Conservative 0; Mismatches 0; Indels 0;
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chromosome 22q11.2; prostate-specific protein; chromosome 1;
prostate specific antigen; PSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate-specific amino acid sequence L1-12/P501S
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                                                                                                                                                        553 AA;
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                                                                                                                                                                                    Query Match
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The present invention describes an isolated polypeptide (PI) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polymuclectides (NI) encoding (PI). (PI) and (NI) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodise from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P77AP, P775P and B305D are located in a genomic region on chromosome 22q1112 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AARH84671 to AAH85143 and AAG99000 to AAG99077 represent polymucleotide and polypeptide sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                  Wang A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 2861; DB 22; Length 553; 100.0%; Pred. No. 2.2e-269; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                   Harlocker SL, Jiang Y,
, Day CH, Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide comprising at least prostate-specific protein, useful in the prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 167-168; 325pp; English.
                                                                                                                                                                                                                                      Xu J, Dillon DC, Mitcham JL, Ha
Kalos MD, Retter MW, Stolk JA,
2000WO-US30904
                                                                  99US-0439313
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les 553; Conservative
                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                    WPI; 2001-308785/32
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481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ 540
 181 IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polymuclectides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the specific proteins and oligonucleotide specific for prostate specific proteins and oligonucleotide that encodes a prostate specific protein are useful polymucleotide that encodes a prostate specific protein are useful for detecting the presence or a cancer or monitoring the progression of a cancer, especially prostate cancer.
                                                                                                                 301 YQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA
                                                                                                                                                                                                                                              421 ASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA
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                                   CCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGEGL
                                                     241 CCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGEGL
                                                                                             YQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate tumour antigen; prostate tumour; therapy; diagnosis; prostate cancer; immunogenic; cytostatic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence for L1-12.
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                    RVVPGRGICLDLAILDSAFILLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes compositions comprising peptides derived from the Wilm's tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a polypeptide described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                        Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
chromosome 11p13; zinc finger transcription factor.
RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ
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; Pred. No. 2.2e-269;
0; Mismatches 0;
                                                                                                                                                                                                                                                                       Human P501S inventive antigen SEQ ID NO: 333.
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Best Local Similarity 100.
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361 AFPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG
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                                                                                                                                                                                                                                  The present invention relates to a new polypeptide comprising an immunogenic portion of a prostate protein. The invention is useful inhibiting the development of prostate cancer in a patient. The invention is also useful as markers for diagnosing prostate cancer for monitoring diseases progression in patients. The present amino acid sequence represents a human prostate tumour protein.
                                                                                                                                                           Novel polypeptides useful as vaccines for inhibiting prostate car
development, comprise an immunogenic portion of prostate protein
                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2861; DB 23;
100.0%; Pred. No. 2.2e-269;
ive 0; Mismatches 0;
                                                                                                                                                                                                        Example 1; Page 59-61; 101pp; English
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ABG76665
ID ABG76665 standard; Protein; 553 AA.
98US-0020956
98US-0030607
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Best Local Similarity 100.
Matches 553; Conservative
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                                           (XUJJ/) XU J.
(DILL/) DILLON D C.
                                                                                                                                                                                                                                                                                                                                     553 AA;
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                                                                                                                  WPI; 2002-642373
N-PSDB; ABS21254
 09-FEB-1998;
25-FEB-1998;
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    sednences
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prostate cancer; cytostatic; vaccine.
 AAH2872, AAB74798 to AAB74821 and AAB74830 are exemplification of the present invention.
                                                                         Length
                                                                                                     Indels
                                                                        ; Score 2861; DB 22;
; Pred. No. 2.2e-269;
0; Mismatches 0;
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                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 553; Conservative 0;
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01-AUG-1997;
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Length 553; Indels

DB 23;

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180 240 240 300 300 360 360 420 420 480 480 540 540

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421 ASSEDSLMTSFLPGFKPGAPFPNGHVGAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ RVVPGRGICLDLAILDSAFILSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ

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YQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA 360
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28-MAR-2001; 2001US-279115P.
02-APR-2001; 2001US-280143P.
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N-PSDB; ABN81324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of detecting prostate cancer by contacting a biological sample from a patient with: (a) a binding agent that binds to a polypeptide having an immunogenic portion of a prostate protein or its variant; (b) 2 oligonucleotide primers, where 1 of the oligonucleotides is specific for a DNA encoding the polypeptide of (a); or (c) an oligonucleotide probe specific for a DNA encoding the polypeptide of (a) polypeptide of (a); polypeptide of (a) with method and polypeptides are useful for diagnosing, treating, particularly by immunotherapy, monitoring the progression, and inhibiting the development of prostate cancer in a patient. The polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76663-ABG76667-AB
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                                                                                                               Human; prostate tumour; immunotherapy; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 65-67; 111pp; English.
                                                                                                                                                                                                                                                                                   97US-0806596.
97US-0904809.
98US-0020747.
                                                                                                                                                                                                                                                    98US-0030606
                                                                                Prostate tumour protein #3
                                               (first entry)
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                                                05-NOV-2002
                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
301 YQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVPSLVMDRLVQRFGTRAVYLASVA
                                                                                                                          AFPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG
                                                                                                                                                                                                                   361 AFPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ
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                                                                                                                                                                                                                                                                                                                                                                      421 ASSEDSLMTSFLPGPKPGPFPNGHVGAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA
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300
for presenting information to identify the relative expression level of (I). (II) is used as a marker to detect, diagnose or identify an allergic response in a patient. The protein can also serve as a target that modulate gene expression or activity and as an antigen to raise polyclonal or monoclonal antibodies. (II) is useful for identifying agents that modulate expression of the protein or agents, such as adonists or antagonists are useful for modulating biological activity and function of (II) and thus are useful for alleviating disease conditions such as allergic hypersensitivity, seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
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                                                                                                                                                                                                                                                             Length 553;
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                                                                                                                                                                                                                                                             100.0%; Score 2861; DB 23;
100.0%; Pred. No. 2.2e-269;
iive 0; Mismatches 0;
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1es 553; Conservative
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patient, useful for diagnosing prostate; cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes

in a cell in a

transcript

Detecting a prostate cancer-associated

WPI; 2002-471335/50. N-PSDB; ABK92217.

are expressed in a prostate tissue

Hevezi P;

Afar D,

Wilson KE,

Mack DH,

Gish KC,

(EOSB-) EOS BIOTECHNOLOGY INC

16-MAR-2001, 2001US-276888P. 06-APR-2001, 2001US-281922P. 24-APR-2001; 2001US-286214P.

2001US-0847046

04-MAY-2001; 2001US-288589P

2000US-0733288 2000US-0733742 2001US-263957P 2001US-276791P

> 08-DEC-2000; 24-JAN-2001;

13-OCT-2000; 08-DEC-2000;

12-OCT-2001; 2001WO-US32045

18-APR-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organisms such as humans or other mammals (e.g. mice, sheep and dogs) The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to methods of detecting a prostate
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100.0%; Pred. No. 2.2e-269;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 553; Conservative
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mammal; cytostatic.

cancer; prostate tumour tissue; human;

Prostate

Mammalia.

WO200230268-A2

Prostate cancer-associated protein #101.

BXSXXXXXXXXXXXXX

(first entry)

15-AUG-2002

ABG61900

ABG61900 standard; Protein; 553 AA

RESULT 14 ABG61900 Kalos MD; Carter D;

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61 PVLGLVCVPLLGSASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDPRPL 120
                                                                                                                                                                                                                                                                                                   The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVQRLWVSRLLRHRKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVQRLWVSRLLRHRKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIG
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                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2861; DB 23; Length 553; 100.0%; Pred. No. 2.2e-269; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                  New prostate-specific polynucleotides for diagnosing and diseases, in particular prostate cancer, and as markers f
                                                                                                                                Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 113; 87pp; English
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Matches 553; Conservative
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WANGA.
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HEPLERWT.
HENDERSONRA.
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STOLK J A.
DAY C H.
VEDVICK T S
CARTER D.
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(STOL/) (DAYC/) (VEDV/) (CART/) ((LISX/) (WANG/) (SKEI/) (HEPL/) (HEDL/) (HEND/) )
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              APPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG
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                                                                                                                                                                                                                                                                                                                 ABB95222 standard; Protein; 553
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09-FEB-1998; 96US-0020956.
23-SEP-1998; 98US-01159812.
15-JAN-1999; 99US-01232149.
09-APR-1999; 99US-0132149.
13-JUL-1999; 99US-0132149.
13-JUL-1999; 99US-0132149.
14-JAN-2000; 2000US-0431672.
14-JAN-2000; 2000US-058857.
09-MAR-2000; 2000US-058857.
09-MAY-2000; 2000US-058857.
09-MAY-2000; 2000US-0588100.
12-MAY-2000; 2000US-0588100.
13-JUN-2000; 2000US-058813.
13-JUN-2000; 2000US-058813.
13-JUN-2000; 2000US-05813.
13-JUN-2000; 2000US-05813.
10-AUG-2000; 2000US-05813.
10-AUG-2000; 2000US-05813.
10-AUG-2000; 2000US-05813.
10-AUG-2000; 2000US-0593793.
29-AUG-2000; 2000US-0593793.
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DILLON D C.
MITCHAM J L.
HARLOCKER S L
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
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(DILL/)
(MITC/)
(HARL/)
(JIAN/)
(KALO/)
(FANG/)
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ABB95222
XX AC ABB95222
XX AC ABB97222
XX ABB97322
XX

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Gaps

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09 9 120 180 180 240 240 300 300 360 360 420 420

480 480

Search completed: December 3, 2003, 17:19:18 Job time : 49 secs

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(without alignments)
2856.916 Million cell updates/sec
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2861
1 MVORLWYSRLLRHRKAQLLL......AIYFATQVVFDKSDLAKYSA
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ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/USO7_NE
/cgn2_6/ptodata/1/pubpaa/USO8_NE
/cgn2_6/ptodata/1/pubpaa/USO8_NE
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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181 IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH 240

Sequence 947, App Sequence 947, App Sequence 974, App Sequence 974, App Sequence 974, App Sequence 1029, App Sequence 708, App Sequence 708, App Sequence 708, App Sequence 708, App Sequence 852, App Sequence 1018, App Sequence 1018, App Sequence 1018, App Sequence 1011, App	VD METHODS FOR THEIR USE	100.0%; Score 2861; DB 9; Length 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0; MVQRLWVSRLLRHRAQLLLVNLLTFGLEVCLAAGITTVPPLLLEVGVEEKFWITWVLGIG 60
US-09-822-827-947 US-09-895-793-947 US-09-895-793-947 US-09-822-827-974 US-09-895-793-974 US-09-895-793-974 US-09-895-793-974 US-09-895-793-708 US-09-789-113-708 US-09-895-793-708 US-09-895-793-708 US-09-895-793-708 US-09-895-793-708 US-09-895-793-708 US-09-785-114-678A-708 US-09-785-114-678A-708 US-09-789-113-708 US-09-789-113-708 US-09-895-814-852 US-09-895-814-852 US-09-895-814-852 US-09-895-814-852 US-09-895-814-852 US-09-895-814-852 US-09-128-852 US-09-895-814-852 US-09-895-814-852 US-09-895-814-852 US-09-128-916-852 US-10-124-678A-1028-916-852 US-10-124-678A-1011 US-10-012-896-1011 US-10-294-025-1011 US-10-294-025-1011	. 60 OF OV	100.0%; Score 2861; DB 9; imilarity 100.0%; Pred. No. 1.9e-245; Conservative 0; Mismatches 0; WQRLWVSRLLRHRRAQLLLVNLLTFGLEVCLAAGITYVI WYQRLWVSRLLRHRRAQLLLVNLLTFGLEVCLAAGITYVI PVLGLVCVPLLGSASDHWRGRYGRRRPFIWALSLGILLS
1000.0 1000.0 1000.0 90.9 59.3 59.3 59.3 59.3 59.3 59.3 59.9 59.9 59.9 69.9 69.5 70.0	101, Application US/097, 101, Application US/097, 102, USZO010018058A1 NT: Reed, Steven G. WT: Xu, Jiangchun WT: Xu, Jiangchun WT: Xu, Jiangchun C. F INVENTION: DAGNOINS I FINVENTION: DIAGNOSIS (FRERNCE 20121.446D1 APPLICATION NUMBER: US/PERENCE 20121.446D1 PILING DATE: 2000-12-13 PRILING DATE:	Similarity 100.0%; Pred 3; Conservative 0; Mi WORLWVSRLLRHRKAQLLLVNLLT WYQRLWVSRLLRHRKAQLLLVNLLT PVLGLVCVPLLGSASDHWRGRYGRR
16 2861 17 2661 19 1696 20 1696 21 1696 22 1696 23 1617.5 24 1417.5 26 1417.5 27 1417.5 28 1417.5 29 1417.5 30 1417.5 31 1403.5 31 1403.5 31 1403.5 32 1403.5 34 1403.5 36 1403.5 37 1403.5 38 1403.5 39 1403.5 39 1403.5 39 1403.5 39 1403.5 40 1197 41 1197 42 1014.5	RESULT 1 Sequence 101, Appli Sequence 101, Appli PREADLICANT: NEGATION APPLICANT: Reed, APPLICANT: NEGATION TITLE OF INVENTION SOFTWARE: FEFERENCE: SEQ ID NO 101 LENGTH: 553 TYPE: PRT ORGANISM: HOMO SEGUENCE: CORRENT APPLICATION CORRENT APPLICATION CORRENT APPLICATION CORRENT APPLICANTON CORRENT APPLICANTON CORRENT FILING DAT NUMBER OF SEQ ID NO 101 TITLE OF TABLE OF	Query Match Best Local Sil Matches 553; Oy 1 M Db 1 M Oy 61 P

480 480 540

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301 YQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA 360
                                                                                                                                           361 AFPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
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181 IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH 240
                                                                                                                                                                                                                                                                                                                                                                   RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
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100.0%; Pred. No. 1.9e-245;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 113, Application US/09759143
Patent No. US2002022248A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Hepler, William
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Best Local Similarity 100.
Matches 553; Conservative
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APPLICANT:
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  ASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPPALCGASACDVSVRVVVGEPTEA
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APPLICANT: Parkes, Debbie
APPLICANT: Schneider, Douglas
APPLICANT: Steinbrecher, Renate
APPLICANT: Steinbrecher, Renate
APPLICANT: Steinbrecher, Renate
APPLICANT: Wu, John
TITLE OF INVENTION: DNA Encoding a No. US20020009455A1e1 PROST 03
TITLE OF INVENTION: DNA Encoding a No. US20020009455A1e1 PROST 03
FILE REFERENCE: 1313.1AUSH
CURRENT APPLICATION NUMBER: US/09/838,785
CURRENT FILING DATE: 2001-04-20
PRIOR PILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 26
SOF ID NOS: 26
SEQ ID NOS: 26
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Patent No. US20020009455Al
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APPLICANT: Lin, Rick
APPLICANT: Parkes, Debbie
APPLICANT: Parry, Gordon
APPLICANT: Schneider, Douglas
APPLICANT: Scheinbrecher, Renate
APPLICANT: Van Heuit, Pam T
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 553; Conserval
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Best Local Similarity
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            BLALLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCRQAYSVYAFMISLGGCLGYLLPA
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APPLICANT: Momeill, Patricia D.
APPLICANT: Houghton, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE FILE REFERENCE: 210121147724
CURRENT APPLICATION WUMBER: US/09/780,669
CURRENT PILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FASLSEQ for With LENGTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 113, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu. Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
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Kalos, Michael D.
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Vedvick, Thomas S
Carter, Darrick
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Retter, Marc W.
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US-09-780-669-113
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100.0%; Score 2861; DB 9; Length 553;

Query Match

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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FC
NUMBER OF SEDUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
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6300 Columbia Center, 701 Fifth Avenue
     Pred. No. 1.9e-245
                           0; Mismatches
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NAME: Maki, David J.
REGISCRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
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Patent No. US20020081580A1
100.08;
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CITY: Seatle
CITY: Seatle
STATE: WA
COUNTRY: USA
TTP: 98104
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; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-822-827-113

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US-09-115-453-113
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FITLE REPERENCE: 210.11.53411
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASISEQ for Windows Version 3.0
                                                                                                                                                                                                                  Length 553;
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                                                                                                                                                                                                                 ; Score 2861; DB 9;
; Pred. No. 1.9e-245;
0; Mismatches 0;
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Patent No. US20020081680A1
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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Best Local Similarity 100.º
Matches 553, Conservative
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US-09-822-827-113
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Query Match
100.0%; Score 2861; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.9e-245;
Matches 553; Conservative 0; Mismatches 0;
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Patent No. US20020090372A1
GENERAL INCAMPATION:
APPLICANT: XW, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR THEIR USE |
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION: METHODS FOR THEIR USE |
CURRENT APPLICATION: MUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
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ORGANISM: Homo sapien
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121-156405 PROSTATE CANCER CURRENT APPLICATION NUMBER: US/09/895,793

CURRENT FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 553
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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Hepler, William T.
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ORGANISM: Homo sapien
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Publication No. US20020182596A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitchan, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C6
CURRENT PRILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE FREEDE FREESEQ for Windows Version 3.0
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100.0%; Score 2861; DB 10; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.9e-245;
Matches 553; Conservative 0; Mismatches 0; Indels 0;
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ORGANISM: Homo sapien
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                                             THE THERAPY
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APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION WNBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF ERQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0)
SEQ ID NO 113
                                                                                                                                                                                                                                                                                                                    100.0%; Score 2861; DB 10;
100.0%; Pred. No. 1.9e-245;
ive 0; Mismatches 0;
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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Best Local Similarity 100.
Matches 553; Conservative
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapien
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US-10-144-678A-113
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                                                                                                              Gaps
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                                                                       Length 553;
                                                                                                            0; Indels
                                                                 Query Match
100.0%; Score 2861; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.9e-245;
Matches 553; Conservative 0; Mismatches 0; 1
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McNeill, Patricia D.
Houghton, Raymond L.
Vinala de Bassols, Carlota
Foy, Teresa
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Publication No. US20020193296A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Ratter, Marc W.
APPLICANT: Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Skeiky, Yasir A.W.
Hepler, William T.
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US-09-895-814-113
                              JS-09-895-793-113
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RESULT 13
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CURRENT APPLICATION NUMBER: US/10/144,678A

CURRENT ILLING DATE: 2002-08-12

NUMBER OF SEQ ID NOS: 1033

SOFTWARE: FastSEQ for Windows Version 3.0
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals Y de Bassols, (
                                                                Wang, Aijun
Skeiky, Yasir A. W.
Hepler, William T.
Hural, John
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Watanabe, Yoshihiro
              Day, Craig H.
Vedvick, Thomas
Carter, Darrick
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Best Local Similarity 100.
Matches 553; Conservative
Stolk, John A.
                                                      Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 13, Application US/10005907
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Sequence 13, Application US/20030166881A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Union Chimique Belge, S.A.
APPLICANT: Discosi, Gregory
APPLICANT: Elistein, Richard
TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ALLERGIC HYPERSENSITIVITY AND MAST CEITILE OF INVENTION: ACTIVATION
FILE REPERENCE: 05329-5605
CURRENT PELICATION NUMBER: US/10/005,907
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 13
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Publication No. US20030185830A1
GENERAL INFORMATION:
APPLICANT: Xu, Jaangchun
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APPLICANT: Stolk, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER FILE REFERENCE: 210121.42729
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastERQ for Windows Version 3.0
SEQ ID NO 113
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                                                                                                                                                                                                                                  Length 553;
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Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Wi, Jiangchun
APPLICANT: Mitcham, Jonnifer L.
APPLICANT: Mitcham, Jonnifer L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Katter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Best Local Similarity 100.
Matches 553; Conservative
                                                                                                                                                    LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                           APPLICANT: Fanger, Gary R.

APPLICANT: Materanbe, Yoshihiro
APPLICANT: Materanbe, Yoshihiro
APPLICANT: Madeleline Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: LORGINGIS OF PROSITE
FILE REFERENCE: 210121.42727
CURRENT APPLICATION WUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 2861; DB 14; Length 553; 100.0%; Pred. No. 1.9e-245; ive 0, Mismatches 0; Indels 0;
                                                                                                                                                           Hural, John
MCNBill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
                                                                               Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553
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Best Local Similarity 100.0
Matches 553; Conservative
                                                            Li, Samuel X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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RVVPGRGICLDLAILDSAFILLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELALLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCRQAYSVYAFMISLGGCLGYLLPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 IDWDTSALAPYLGTQEECLFGLITLIFLTCVAATLLVAREAALGPTEPARGLSAPSLSPH 240
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                                                                                                                                                                        APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Ralos, Wichael
APPLICANT: Ralos, Michael
APPLICANT: Ralos, Michael
APPLICANT: Ralos, Michael
APPLICANT: Ralos, Michael
APPLICANT: Retter, Mark
APPLICANT: Rolls, John
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.4.27D3
CURRENT PAPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 113
***CENTANTE FARENCE: PARENCE: PA
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100.0%; Score 2861; DB 15; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.9e-245;
Matches 553; Conservative 0; Mismatches 0; Indels 0;
VVFDKSDLAKYSA 553
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TYPE: PRT
ORGANISM: Homo sapien
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Search completed: December 3, 2003, 17:22:03 Job time: 37 secs

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5.1.6	Compugen Ltd.
version	- 2003
GenCore	(c) 1993
	Copyright

- protein search, using sw model OM protein December 3, 2003, 17:17:41; Search time 21 Seconds (without alignments) 2532.442 Million cell updates/sec Run on:

US-09-593-793A-113 2861 score: Title: Perfect so Sequence:

1 MVQRLWVSRLLRHRKAQLLL......AIYFATQVVFDKSDLAKYSA

BLOSUM62 Gapoxt 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB e Maximum DB e

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:* Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

17;

79; Gaps

DB 2; Length 515; Indels

Ouery Match 12.1%; Score 347.5; DB 2; Best Local Similarity 25.9%; Pred. No. 1e-18; Matches 131; Conservative 80; Mismatches 215;

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94 93 94 HCQSSFGRRRPFIASGAGCVAISVILI---GFAADISYKAGDDMSKTLKPRAVTVFVIGF 150

77 HWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGL-----LCPDPRPLELALLILGV

:|:|| : |:: |:: |:: |:: || 34 KLVLVAAIAAGVQFGWALQLSLLTPYVQLLGIPHKWAAYIWLCGPISGMLVQPIVGYYSD 17 QLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIGPVLGLVCVPLLGSASD

179 PAIDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLS 211 PFS--KTHACDLYCANLKSCFIISIALLIIITVVALSVVRENS--GPPDDADAAEEP---239 PHCCPCRARLAFRNLGALLPRIHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGE

셤 ð

Š ద ð g 8

130 GLLDFCGQVCFTFLEALLSDLFR-DPDHCRQAYSVYAFMISLGGCLGY-----LL

299 GLYQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLAS 358

264 ----PSSGKIPV--FGELLGALKDL----PRPMLLLLLVTCLNWIAWFPFILFDTDWMGR 313

367 FVNFILAIGLVMTVVVSKVAQHQREHSANGQLLPPSAGVKAGALSLFSILGIPLSITYSI 426

359 VAAFPVAAGATCL-----SHSV-----AVVTASA----ALTGFTFSALQIL 395

178

238 263 298

Description	sucrose-proton tra	sucrose transport	sucrose transport	probable sucrose-p	13	sucrose transport	probable sucrose-p	sucrose transport	sucrose transport	sucrose-proton tra	sucrose transport	sucrose transport	sucrose-proton sym	probable sucrose t	probable sucrose t	hypothetical prote	probable sucrose-p	sucrose transport	probable sucrose-p	sucrose transport	probable sucrose c	hypothetical prote			hypothetical prote	14	membrane protein,		MFS
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SUMMARIES	T14340	T12198	JQ2389	384441	S28052	838196	G86360	S48789	843142	T14339	S48788	S38657	S51114	F96741	T02982	A86234	E96691	S38197	A84520	852377	T38541	F75217	B87532	875696	A75444	E75217	B87536	G83413	3503
#	: #	Ħ	5	89	S	83	89	S	S	Ţ	S	S	S	F 9	Ę.	A8	8	S	A8	SS	13	F7	B 8	S	A7	日	BB	89	G83
DB	7	~	7	7	Ŋ	7	7	7	7	7	7	7	N	~	~	N	N	~	N	N	0	N	~	7	~	7	~	7	7
Length	515	523	516	594	525	512	512	507	533	501	428	510	523	512	537	474	491	513	492	503	553	452	541	544	454	430	418	389	422
, % Query Match	12.1	•	11.5		11.3	11.3	11.3	11.1	10.9	10.7	10.4	10.3	10.3	10.2			٠	9. 8.	•	9.5	8.2		9.9	5.0	4.9	4.8	4.8	4.6	4.5
Score	7	337.5	330	328.5	324.5	323,5	323.5	317.5	311	305.5	297.5	294	294	292.5	292	286	281.5,	279.5	276.5	273	235.5	191	187.5	142	139.5	138.5	136	~	128.5
Result No.	-	7	ю	4	ស	ø	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	29

	٠.	108 K	4 L	7.94	c	. 90000	opeomyor oldedova
	3.5	127.5	. 4	472	۱ ۵	F82639	resistance protein
	32	127	4.	451		E81781	probable integral
	33	126	4.4	394	7	AB3073	tetracycline řesis
	34	126	4.4	394	~	G98213	drug efflux protei
	32	126	4.4	451	~	A81206	sugar transporter,
	36	125.5	4.4	399	N	JQ1479	
	37	125	4.4	391	~	S74688	hypothetical prote
	38	125	4.4	407	7	H75515	tetracycline-efflu
	39	124.5	4.4	399	٦	838656	tetA protein - Pse
	40	123.5	4.3	400	7	AG2866	MPS permease [drug
	41	123.5	4.3	400	~	D97643	probable efflux pr
	42	123	4.3	440	~	AD0986	hypothetical metab
	43	121.5	4.2	398	0	C90349	multidrug-efflux t
	44	121.5	4.2	503	7	843017	puromycin resistan
	45	121	4.2	483	0	AF2363	hypothetical prote
						ALIGNMENTS	
	RESULT 1						
	T14340						
	Sucrose N:Alter	sucrose-proton transport protein - N:Alternate names: sucrose/H+ sympo	ransport S: Sucro	prot	ein	sucrose-proton transport protein - carrot N:Alternate names: sucrose/H+ symporter protein	
	C;Specie	C;Species: Daucus carota (carrot)	s carota	(car	rot)		
٠.	C;Date:	C;Date: 20-Sep-1999	999 #seq	nence	rev	C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #1	<pre>#text_change 21-Jul-2000</pre>
. <i>.</i>	R:Shakve	R:Shakva, R.: Sturm, A.	urm. A.				
	Plant Ph	Plant Physiol. 118, 1473-1480, 1998	18, 1473	-1480	13	86	
	A;Title:	. Charact	erizatio	n of	Bour	ce- and sink-specif:	A; Title: Characterization of source- and sink-specific sucrose/H+ symporters from carrot
΄.	A, Refere	ance numb	er: Z179	91; M	din:	A, Reference number: Z17991; MUID:99063785; PMID:9847123	
	A; Accest	A; Accession: T14340	340	•			
,	A;Status	A;Status: preliminary A:Wolecule type: mpNA	inary; t	ransl	ated	A; Status: preliminary; translated from GB/EMBL/DDBJ	
	A.Residu	A:Residues: 1-515 <sha></sha>	5 <sha></sha>				
	A, Cross	reference	es: EMBL	Y167	68;		PIDN:CAA76369.1; PID:g2969884
	A; Experimental	mental s	onrce: c	atatn	a r	source: cultivar Namtaise; root	
,	A;Note: SUT2	SUTZ				_	
	C; Superi	Eamily: Co	ommon to	bacco	Bac	C; Superfamily: common tobacco sucrose transport protein	ain

N

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C;Accession: JQ2389; S40310
R;Riesmeier, J W.; Hinner, B.; Frommer, W.B.
Plant Cell 5, 1591-1598, 1993
A;Title: Potato sucrose transporter expression in minor veins indicates a role in phloem A;Reference number: JQ2389; MUID:94146554; PMID:8312741
A;Accession: JQ2389
A;Accession: JQ2389
A;Accession: JQ2389
A;Accession: JQ2389
A;Residues: 1-516 <RIE>
A;Residues: 1-516 <RIE>
A;Experimental source: Cv. Desiree
C;Comment: The gene encoding for this protein is highly expressed in mature leaves.
C;Superfamily: common tobacco sucrose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 YLLPAIDW------DTSALAPYLGTQEECLF-GLLTLIFLTCVAATLLVAEE-AALGP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 TEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMAL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|| ::::| : || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 GLVCVPLLGSASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGL-----LCPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 PRPLELALLILGVGLLDFCGQVCFTPLEALLSDLFRDPD-HCRQAYSVYAFMISLGGCLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 YAAGSYSHLFKVFPFSKTKACDMYCANLKSCFFIAIFLLLSLTTIALTLVRENELPEKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 MIFILFYIDFVGEGLYQGVPRAEPGIEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 VQRFGTRAVYLASVAAFPVAAGATCLSHSVAVV------TASAALTGFT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: | | | : | : | | | : | 356 GKKIG-GAKRLAGTLMGPT-AICLAMTILVTKWAEKSRQHDPAGTLMGPTPGVKIGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 --FSALQI-----LPYTLASLYHREK------QVFLPKYRGDTGGASSEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 LLFAALGIPLAATFSIPFALASIFSSNRGSGOGLSLGVLNLAIVVPQMLVSLVGGPWDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 RLWVSRLLRHRKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIGPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 IMTSFLPGPKPGAPFPNGHVGAGGSG------LLLPPPPALCGASACDVSVRVVVG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.5%; Score 330; DB 2; Length 516; Best Local Similarity 24.7%; Pred. No. 2.2e-17; Matches 132; Conservative 93; Mismatches 197; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,331-349/Domain: transmembrane #status predicted <TW8>
'366-385/Domain: transmembrane #status predicted <TW9>
'409-9427/Domain: transmembrane #status predicted <TW10>
'429-448/Domain: transmembrane #status predicted <TW10>
'32,9248/Domain: transmembrane #status predicted <TW11>
'33,92/Binding site: carbohydrate (Asn) (covalent) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hatatus predicted <TM5>
Hatatus predicted <TM6>
Hatatus predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;103-122/Domain: transmembrane #status predicted <TM3>
F;141-160/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reywords: glycoprotein; transmembrane protein
131-53/Domain: transmembrane #status predicted <TMl>
67-86/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGGGNLPG-----FVVGAVAAAASAVLALTMLPSPPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane #
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;141-160/Domain:
F;180-200/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;226-248/Domain:
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                                                                                                                                                                                                                                                                                                                                                                        Sucrose transport protein - fava bean
C;Species: Vicia faba (fava bean)
C;Species: Vicia faba (fava bean)
C;Species: Vicia faba (fava bean)
C;Date: 23-Uul-1999 #sequence_revision 23-Jul-1999 #text_change 20-Jun-2000
C;Accession: T12198
R;Weber, H.; Borisjuk, L.; Heim, U.; Sauer, N.; Wobus, U.
R;Weber, H.; Borisjuk, L.; Heim, U.; Sauer, N.; Wobus, U.
A;Title: A role for sugar transporters during seed development: molecular characterizati
A;Reference number: Z17451; MUD:97355984; PMID:9212465
A;Accession: T12198
A;Accession: T12198
A;Accession: T12198
A;Residues: Preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-523 <WEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                  212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 HWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGL-----LCPDPRPLELALLILGV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 GLIDPCGOVCFTPLEALLSDLFR-DPDHCROAYSVYAFMISLGGCLGYLLPAID----- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 SLSPHCCPCRARL--AFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFVGEGLYQGVPRAEPGTEARRH-YDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTR 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 VKRĽWGIVNFLL---ÀICĽGLTVLVTKLAQHSRQYAPGTGALGDPLPPSEGIKAGALTLF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SSTSGAGQGLSLGVLNLAIVIPQMFVS 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 KIMVVASIAAGVQPGWALQLSLLTPYVQLLGIHHTWAAYIWLCGPISGMLVQPIVGYHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --WDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLV-AEEAALGPTEPA---BGLSAP
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; Pred. No. 5.9e-18;
76; Mismatches 185; Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFSALQI ----LPYTLASLYHREKQVFLPKYRGDTGGASSEDSL
       PYTLASLYHREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LLPPPP 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 VLSGPWDALFGGGNLPAFVVGAVAALASGILSIILLPSPP 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: sut
C;Superfamily: common tobacco sucrose transport protein
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                                                                                                                                                 449 GGSGLLP----PPPALCGASACDVS 469
                                                                                                                                                                                                                  487 AISGVLAIVLLPKPSKDAASKLSLS 511
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25.8%;
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 25.8*
Matches 134; Conservative
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Arabidopsis thaliana

G84441 probable sucrose-proton symporter [imported] - Ar C.Species: Arabidopsis thaliana (mouse-ear cress)

> JQ2389 sucrose transport protein - potato

20;

Gaps

74 94

C;Genetics

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A; Molecule type: mRNA
A; Residues: 1-512 < SAU>
A; Crost States: 1-512 < SAUS
A; Crost States: 1-522 < SAUS
A; Crost States: 1-522 < SAUS
A; Crost States: 1-522 < Crost States: 1-5222 < Crot States: 1-5
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Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cjate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Dec-2000
CjAccession: S38196; T00773
Risauer, N.K.
Risauer, N.K.
Alberription: SUC1 and SUC2: two sucrose transporters from Arabidopsis thaliana.
Alberription: SUC1 and SUC2: two sucrose transporters from Arabidopsis thaliana.
Alacession: S38196
                                                                                                                                                                                                                                                                                                                                                                                                                                               SDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLA-GLLCPDP-----RPLELALLIL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----WDTSALAPYLGTQEECLFGLLT-LIFLTCVAATTLVAEEAALGPTEPAEGLSAPSL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 VFPFTKTAACDVYCANLKSCFFISITLLIVLTILALSVVKERQITIDBIQEBEDLKNRNN 271
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                                                                                                                                                                                                                                                                                                   23 LLTFGLEVCLAAGITY-----VPPLLLEVGVEEKFMTMVLGIGPVLGLVCVPLLGSA
                                                                                                                                                                                                                                                                                                                                                        35 LKKLGLVASVAAGVQFGWALQLSLLTPYVQLLGIPHTWAAYIWLCGPISGMIVQPLVGYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 GFWILDVANNTLOGPCRALLADMAAGSQTKTRYANAFFSFFMALGNIGGYAAGSYSRLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----HFRDSHHIM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 GDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPALCGASACDVSVRVVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GSAVPPPPPA--GVKGGALAIFAVLG
       A;Cross-references: EMBL:X67125; NID:g21318; PIDN:CAA47604.1; PID:g21319
                                                                                                                                                                                                                           Indels 141;
                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 EPTEARV-VP------GRGICLDLAILDSAFLLSQV---
                                         C, Superfamily: common tobacco sucrose transport protein C, Keywords: transmembrane protein
                                                                                                                                                   11.3%; Score 324.5; DB 2; 23.2%; Pred. No. 5.8e-17; tive 91; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sucrose transport protein SUC2 - Arabidopsis thaliana
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490 AFVVGAVAATASAVLSF 506
                                                                                                                                                                                     Best Local Similarity 23.2
Matches 129; Conservative
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                                                                                                                                                       Query Match
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                      C. Accession: G8441

R. Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R. Lin, X.; Kaul, S.; Rounsley, S.D.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 functi
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NyAlternate names: sucrose carrier protein; sucrose permease
C;Species: Spinacia oleracea (spinach)
C;Species: Spinacia oleracea (spinach)
C;Date: 17.Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jul-2000
C;Accession: S28052
R;Risemeier, J.W.; willmitzer, L.; Frommer, W.B.
R;Risemeier, J.W.; willmitzer, L.; Frommer, W.B.
A;Title: Isolation and characterization of a sucrose carrier cDNA from spinach by :
A;Reference number: S28052; MUD:93099843; PMID:1464305
A;Rocession: S28052
A;Rocession: S28052
A;Rocession: S28052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLA--GLLCPD------PRPLE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 TRIQDSAPLLDD------LQSKGLEHSKLNNGTANGIKYERVERDTDEQFGNSENEHQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVY-LASVAAFPV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 AAGATCLS--------HOVAVVTASAALTGFTFSALQILPYTLASLY 403
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                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-594 <STO>
A;Cross-references: GB;AE002093; NID:g3461813; PIDN:AAC32907.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLLTFGLEVCLAAGITY------VPPLLLEVGVEEKFMTMVLGIGPVLGLVCVPLLGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.5%; Score 328.5; DB 2; Length 594; Best Local Similarity 24.1%; Pred. No. 3.3e-17; Matches 120; Conservative 72; Mismatches 174; Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 2
C,Superfamily: common tobacco sucrose transport protein
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-----EVTADSGG 522
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                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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A,Map position: 1
C,Superfamily: common tobacco sucrose transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: S48789
A;Status: preliminary
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Best Local Simil
Matches 123; (
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Best Local Simi
Matches 125; (
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C, Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
C, Accession: G86360
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, W.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Alathors: Huizar, J.C.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A, Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Reference and analysis of chromosome lof the plant Arabidopsis.
A, Accession: G86360
A, Status: preliminary
A, Molecule type: DNA
A, Conseries of Carcon-come loft the content of the con
A;Cross-references: EMBL:AC003979; NID:g3172156; PID:g3287687; GSPDB:GN00059; ATSP:T22J1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: SUC2; ATSP:T22J18.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGL-----LCPDPRPLELALLI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGVGLLDFCGQVCFTPLEALLSDLFR-DPDHCRQAYSVYAFMISLGGCLGY-----LL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 KVVPFTMTESCDLYCANLKTCFFLSITLL-LIVTFVSLCYVKEKPWTPEPTADGKA---- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAIDWD-TSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 EGLYQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIVNFIL---AICLAMTVVVTKQAENHRRDHGGAKTGPPGNVTAGALTLFAILGIPQAIT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSALOILPYTLASLYHREK------QVFLPKYRGDTGGASSEDSLMTSFLPGP 435
                                                                                                                                                                                                                                                                                                                                                                                   14 RKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIGPVLGLYCVPLLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPHCCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVG
                                                                                                                                                                                                                                                                                              92; Mismatches 195; Indels 101;
                                                                                                                                                                                                                                          11.3%; Score 323.5; DB 2; Length 512; 24.1%; Pred. No. 6.7e-17;
                                                                                                       A,Map position: 1
A;Introns: 419/3; 441/1; 455/3
C;Superfamily: common tobacco sucrose transport protein
C;Keywords: sugar transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----FVLGAIAAAVSGVLGLTVLPSPPPA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 KPGAPPPNGHVGAGGSGLL-----PPPPA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVAAFPVAAGATCLSHSVAV----
                                                                                                                                                                                                                                                                      Best Local Similarity 24.13
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
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18;
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                                                                                                                                                                                                                                                                                                                                                                                      237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 SPHCCPCRARLAFRNIGALLPRIHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 EGLYQCVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --VTASA----ALTG----FT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 GMIVQPVVĞYYSDNCSSRFGRRRGFIAAGAALVTIAVFLIGFAADL-GHATGDPLGKGSK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 PLELALLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCRQAYSVYAFMISLGGCLGYLL 178
                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sucrose transport protein - common tobacco |
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ::: |: :: |:: |:: |:: | SERKIISVSSIAAGVQFGWALQLSLTFYVQLLGIPHKWASLIWLCGPISGMLVQPIVGY
                                                                                                                     14 RKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIGPVLGLVCVPLLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 PAIDWD-TSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 GIVNFIL---AICLAMTVVVTKQAENHRRDHGGAKTGPPGNVTAGALTLFAILGIPQAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 RLWVSRLLRHRKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIGPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GLVCVPLLGSASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDP-
                                                             101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99;
        Length 512;
                                                             Indels
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C;Superfamily: common tobacco sucrose transport protein
11.3%; Score 323.5; DB 2; ilarity 24.1%; Pred. No. 6.7e-17; Conservative 92; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.1%; Score 317.5; DB 2;
llarity 24.3%; Pred. No. 1.9e-16;
Conservative 87; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 KPGAPFPNGHVGAGGSGLL-----PPPPA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FVLGAIAAAVSGVLALTVLPSPPDA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S48789
R;Buerkle, X.Y.Z.; Frommer, W.B.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 SVAAFPVAAGATCLSHSVAV--------
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: :: :	OY 354 VYLASVAAFPVAAGATCLSHSVAVVTASAALITGFTFSALQILPYTLASLYHREKQVFLPK 413
Qy 179 PAIDWDISALAFYLGTQEBCLF-GLLTLIFLITCVARTLLVAEBAALGFTEFA 229 :	Db 376 KRLMGIVNFVLAVCLAMTV-LVTKQABST
Qy 230 EGLSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPRTLFRLFVAELCSWMALMTFT 289 OSO RTDERAGANESKYUDE, EPETEGALKUT DDDMWTTILIMPGH MWTADEDDE 207	406
290 LFYTDFVGEGLYQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRF	MGVPQAITYSIPFALASIFSNTSGAGGGLSLGVLALSIVIPQAITYSIPFALASIFSNTSGAGGGLSLGVLALSIVIPQAITYSIPFALASIFSNTSGAGGGLSLGVLALSIVIPQAITVSVAAGPWDALFGGGN 49
Db 298 LYDTDWMAKEVYGGKVGDGRLYDLGVHAGALGLLLNSVVLGFMSLSVBFLGKKI 351 Oy 350 GTRAVYLASVAAFPVAAGATCLSHSVAVVTASAALTGFTFSALQI 394 Db 350 GTRAVIASVAAFPVAAGATCLSHSVAVV	Oy 520 VTAYMYSAAGLGLVAIYPATQVVFDKSDLAKYSA 553
395	RESULT 10 T14339 Bucrose-proton transport protein - carrot N'Alternate names: sucrose/H+ symporter protein
	C;Species: Daucus carota (carrot) C;Date: 20-58p-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C;Accession: T14339 R;Shakya, R.; Sturm, A.
RESULT 9 S43142	Fight Fnysiol. 118, 14/3-1480, 1998 A;Title: Characterization of source- and sink-specific sucrose/H+ symporters from carrot A;Reference number: Z17991; MUID:99063785; PMID:9847123 A;Accession: T14339
sucrose transport protein - castor bean N;Alternate names: sucrose carrier C;Species: Ricinus communis (castor bean) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-May-2000	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-501 <sha> A;Residues: 1-501 <sha> A;Cross-references: EMBL:Y16766; NID:g2969886; PIDN:CAA76367.1; PID:g2969887</sha></sha>
C.Accession: S43142 R;Weigy, A.; Komor, E. R;Weited to the EMBL Data Library, March 1994 A;Description: A sucrose carrier from Ricinus communis.	A;Experimental source: cultivar Namtaise: leaf C;Genetics: A;Gene: SUTia C;Superfamily: common tobacco sucrose transport protein
Arceesion: Number: 543142 Arceesion: S43142 Arceesion: Status: preliminary Armolecule type: mRNA	Query Match Best Local Similarity 21.6%; Pred. No. 1.5e-15; Matches 124; Conservative 91; Mismatches 213; Indels 145; Gaps 14;
Arkesloues: 1-533 <wel> Arcross-references: EMBL:231561; NID:g468561; PID:g468562 C;Superfamily: common tobacco sucrose transport protein</wel>	Qy 18 LLLVNLLFRGLEVCLAAGITYVPPLLLEVGVEEKRMTWLGIGPVLGLVCVPLLGSASDH 77
Query Match Best Local Similarity 23.3%; Pred. No. 6.2e-16; Matches 134; Conservative 95; Mismatches 225; Indels 120; Gaps 19;	78 WRGRYGRRRPPIWALSLGILLSLFLIPRAGWLAGLCPDPRPLELALLILGVGLIDFC 1
Cy 17 QLLLVNLLTPGLEVCLAAGITYVPPLLLEVGVEEKPMTMVLGIGPVLGLVCVPLLGSASD 76	136 GQVCFTPLEALLSDLF-RDPDHCRQAYSVYAFMISLGGCLGYLLPAIDWDTSALAPYLGT
OY 77 HWRCRYGRRRPFIWALSLGILLSLPLIPRAGWLAG-LLCPDPRPLELALLILGVGLL 132 Db 97 RCTSRFGRRRPFIASGAAFVAIAVFLIGYAADLGHLSGDSLDKSFKTRAIAIFVVGFWIL 156	OY 195 QBECLFGLTLIFFTCVAATLLVAERAALGTEPAEGL 232
Qy 133 DFCGQVCFTPLEALLSDLF-RDPDHCRQAYSVYAFMISLGGCLGYLLPAIDW 183	233 SAPSLSPHCEPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLFY 23 CAN COLL TO THE TOTAL THE T
QY 184 DTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAP 235 bb 217 KTTACDVYCANLKSCFFISIVLLSLTVLALSYVKEKPWSPDQAVDNAEDDTASQA 272	293 TDFVGEGLYQGVPRAEPGTEARRHYDEGVRMGSLGLFFLGVRUVLLLYVPSLVMDILVQRFGTR
QY 236 SLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSHMALMTFTLFYT 293 Db 273 SSSAQPMPFFGEILGAFRAL	306 TDWMGREIYGGEPNQQQSYSDGVRMGAFGLMMNSVVLGITSVLMEKLCRIWGSG 353 AVYLASVAAFPVAAGAICLSHSVAVVIASAALIGFTFSALQILPYILASLYHREKQVFLP :: : :: :: :: ::
Qy 294 DFVGEGLYQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRA 353 	Db 360 FMW 388 Qy 413 KYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPPALCGASACDVSVRV 472

A; Reference number: 838657 A; Accession: 638657 A; Accession: 538657 A; Rolecule type: mRNA A; Residues: 1-510 < GAH> A; Cross-references: EMBL:X75764; NID:g415987; PIDN:CAA53390.1; PID:g415988 C; Ganetics: A; Gene: ptpl C; Superfamily: common tobacco sucrose transport protein C; Keywords: sugar transport	Query Match Best Local Similarity 24.7%; Pred. No. 1.18-14; Bast Local Similarity 24.18-14; Bast Local Similarity 24.18-18; Bast Local Similar	RESULT 13 S51114 S51114 S51114 Scrose-proton symporter - beet C, Species: Beta vulgaris (beet) C; Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 26-May-2000 C; Accession: S51114 R; Westram, A.; Bckhardt, U.; Frommer, W.B.; Riesmeier, J.W. Submitted to the EMBL Data Library, January 1995 A; Description: Sequence of a sugar beet sucrose transporter cDNA. A; Reference number: S51114 A; Accession: S51114 A; Accession: S51114 A; Reference mumber: S51114 A; Reference mumber: S51114 A; Residues: 1-523 - WBS. A; Ccoss-references: EMBL: X83850; NID:g633171; PID:g633172 C; Superfamily: common tobacco sucrose transport protein Query Match Query Match Best Local Similarity 24.3%; Pred. No. 1.2e-14; Best Local Similarity 24.3%; Pred. No. 1.2e-14; Matches 125; Conservative 78; Mismatches 199; Indels 112; Gaps 20; Cy 17 QLLLVNLLIFGLEVCLAAGITYVPPLLLEVGVEEKFWITWVLGIGPVLGLVCVPLLGSSASD 76
Db 389	RESULT 1.1 SA8788 SUCTOBE transport protein - tomato (fragment) C.\$Pecis: Divopersion esculentum (comato) C.\$Accession: SA8788 R.Buerkle, X.Y.Z.; Prommer, W.B. A.R.Cassion: SA8788 A.A.Cassion: SA87888 A.A.Cassion: SA878888 A.A.Cassion: SA878888 A.A.Cassion: SA878888 A.A.Cassion: SA8788888 A.A.Cassion: SA87888888 A.A.Cassion: SA87888888 A.A.Cassion: SA87888888 A.A.Cassion: SA87888888 A.A.Cassion: SA878888888 A.A.Cassion: SA878888888 A.A.Cassion: SA8788888888 A.A.Cassion: SA87888888888888 A.A.Cassion: SA878888888888888 A.A.Cassion: SA8788888888888888888888888888888888888	Oy 285 IMTFTLFYTDFVGEGLYQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDR 344 Db 297 WFPFLYDTDWMAKEVFGGQVGDAKLYDLGVRAGALGLLLQSVVLGFMSLGVFF 350 Qy 345 LVQRFGTRAVYLASVAAFPVAAGATCLSHSVAVVTASAALTGFT 388

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8 g

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probable sucrose transport protein - rice
(Species: Oryza sativa (rice)
C,Species: Oryza sativa (rice)
C,Accession: T02982
R;Hirose, T.; Inaizumi, N.; Scofield, G.N.; Furbank, R.T.; Ohsugi, R.
Plant Cell Physiol. 38, 1389-1396, 1997
A;Title: cDNA cloning and tissue specific expression of a gene for sucrose transporter in A;Reference number: Z14809; MUID:98182940; PMID:9522469
                                                                                                                                                                                                                                                                                                                                263
                                                                                                                                                                                                                                                                                                                                                                                                                298
        RCESRFGRRRPFIAAGVALVAVSVFLI---GFAADMGHSFGDKLENKVRTRAIIIFLTGF 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 -----SLFF--FGEIFGAVR----HMKRPMVMLLIVIVINWIAWFPFILYDTDWMGR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 GLYQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLAS 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| | :: :::||:||| : :::||| | | 310 EVYGG--NSDGDERSKKLYDQGVQAGALGLMFNSILLGFVSLGVESIGRKMG-GAKRLWG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 CVNFILAIG---LAMTVLVTKSAEHHREIAGPLAGPSSGIKAGVFSLFTVLGIPLAITYS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 HWRGRYGRRRPFIWALSLGILLSLFLI---PRAGWLAGLLCPD-----PRPLELALLIL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVGLLDFCGQVCFTPLEALLSDLF--RDPDHCRQAYSVYAFMISLGGCLGYLLPAID--- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9/
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-537 <ARNA
A,Residues: 1-537 <ARNA
A,Cross-references: EMBL:D87819; NID:g2723470; PIDN:BAA24071.1; PID:g2723471
A,Experimental source: cultivar Nipponbare, leaf
                                                                                                                                                                                                                                                                                                       210 PFT--MTKACDIYCANLKTCFFLSITLLLIVTFSSLWYVKDK----QWSPPQGDKEEKTS
                                                                                                                                                              150 WFLDVANNTLOGPCRAFLADLAAGDAKKTRVANACFSFFMAVGNVLGYAAGSYTNLHKMF
                                                                                                                                                                                                                                                 PAIDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATULVAEEAALGPTEPAEGLSAPSLS
                                                                                                                                                                                                                                                                                                                                                                                                            PHCCPCRARLAFRNLGALLPRIHOLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 -PYTLASLYHREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKP----GAPFPN---GHVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 GFWLLDFSNNTVQGPARALMADLSGRHGPG---TANSIFCSWMAMGNILGYSSGSTNNWH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 KW-----PPFLKTRACCEACANLKGAFLVAVIFLSLCLVITLIFAKEVPFKGNAAL-PTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>::</del>
-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 VAAFPVAAGATCLSHSVAVVTA-----SAALTGFTFSALQIL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
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                                                                                       GLLDFCGQVCFTPLEALLSDLFR-DPDHCRQAYSVYAFMISLGGCLGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: common tobacco sucrose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PPP--PALCGA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 AAVSGVLALTVLPSPPPDAPAMSGA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity ....
Matches 115; Conservative
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        93
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O.2.Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: F96741
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Ii, Y.; Liu, X.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FT--HTKACDIYCANLKSCFFISITLLIVLTILALSVVRER----PFTLDBIQEEENLKN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: | | |: :: :|| || || NLIL-----AVCLAMTI-LVTKSAEHYRATHHVPGAIGPPLPPPGVKGGALAIFAVLGI 428
                                                                                                                77 HWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLA--GLLCPD-----PRPLELALLILGV 129
                                                                                                                                                                      ::||| ||| ::| | | ::| | STREET | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::|
                                                                                                                                                                                                                                                                                                                                                         155 WILDVANNTLOGPCRALLADMAAGSQAKTRYANAFFSFFMALGNIGGYAGSYGRLYTVFP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                         180 AIDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCCPCRARLAFRNLGALLPRIHQLCCRMPRTLRRLFVABLCSWMALMTFTLFYTDFVGEG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFG--TRAVYLA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ALTGF 387
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A;Residues: 1-512 <STO>
A;Cross-references: GB:AE005173; NID:g6978914; PIDN:AAF34306.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                              GLLDFCGQVCFTPLEALLSDLFRDPD-HCRQAYSVYAFMISLGGCLGY-----LLP
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10.2%; Score 292.5; DB 2; Length 5
Best Local Similarity 23.8%; Pred. No. 1.5e-14;
Matches 120; Conservative 87; Mismatches 211; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFLPGPKPGAPFPNGHVGAGGSG-----LLPPPP
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Db 321 WFPFILYDTDWMGREIYHGDPKGTDPQIEAFNQGVRAGAFGLLLNSIVLGFSSFLIE 377 Qy 344 RLVQRFGTRAVYLASVAAFPVAAGATCLSHSVAVVTASAALTGFTFSALQ 393 Db 378 PMCRKVGFRVWVTSNFLVCIAMAATALISFWSLKDFHGTVQKAITADKSIKAVCLVLFA 437 Qy 394 ILPYTLASLY 403 Db 438 FLGVPLAVLY 447

Search completed: December 3, 2003, 17:21:14 Job time : 22 secs

OM protein - protein search, using sw model

December 3, 2003, 17:16:16; Search time 18 Seconds (without alignments) 1444.765 Million cell updates/sec Run on:

Title: Perfect score:

US-09-593-793A-113 2861 1 MVQRLWVSRLLRHRKAQLLĽ......AIYFATQVVFDKSDLAKYSA Sequence:

Scoring table:

BLOSUM62 F. Gapext 0.5

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	99umx9 homo sapien Q93411 spinacia ol Q14091 schizosacch P74168 synechocyst O95528 homo sapien P02982 escherichia P42670 streptcomyce P36670 escherichia P37594 salmonalla Q10880 mycobacteri O24731 nocardioide Q03692 homo sapien Q60755 homo sapien Q60755 homo sapien Q60755 homo sapien Q50720 rhodobacter P2482 pseudomonas P47159 saccharcomyc P30878 salmonella Q50186 mycobacteri P76350 escherichia P625185 pseudomonas Q82ch3 yersilius su Q82ch3 yersilius pe P25185 pseudomonas Q02581 homo sapien Q93704 streptomyce
SUMMARIES	MATP MOUSE MATP HUMAN STP_SCHOOL SUT_SCHOOL SUT_SCHOOL TCR1_ECOLI PURB_ECOLI PURB_ECOLI SWAP_SALTY WHJE_ECOLI SWAP_SALTY WHJE_ECOLI SWAP_SALTY WHJE_ECOLI SWAP_SALTY WHJE_ECOLI SWAP_SALTY WHJE_ECOLI SWAP_SALTY CALA_HUMAN WOCC_THETH SPHZ_HUMAN WOCC_THETH SPHZ_HUMAN WOCC_THETH SPHZ_HUMAN WOCC_THETH SPHZ_HUMAN WOCC_THETH SPHZ_HUMAN WOCC_THETH SPHZ_HUMAN WALLE_SALTY WELE_SALTY WHIS_KLEPN WHJE_SUTY WHYM_RHISN WHYM WHYM WHYM WHYM WHYM WHYM WHYM WHYM
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Score	4888.5 324.5 324.5 142.5 142.5 142.5 1121.5 1121.5 1101.5 1100.1 100.1 100.1 101.5 101.5 102.5 101.5 101.5 102.5 101.5 101.5 102.5 101.5 1
Result No.	

	F3360/ escuericura	O87656 salmonella	079451 sorex ciner	P28568 gallus gall	Q9evn4 pseudomonas	P79393 bos taurus	034245 wolinella s	Q02846 homo sapien	079452 sorex hayde	079969 sorex monti		088626 rattus norv	
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,	7.7	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	
6	20.0	98.5	96	86	97.5	97.5	97.5	97.5	97	97	97	97	
;	4,0	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 MATP MOUSE

	530 AA.	ed) sequence update)	28-FEB-2003 (Rel. 41, Last annotation update) Membrane-associated transporter protein (AIM-1 protein) (Melanoma			Craniata; Vertebrata; Buteleostomi;	Sciurognathi; Muridae; Murinae; Mus.			and Uterus;		novel transporter protein, reduce	-		R ASN-153 AND PRO-435.		N., Gardner J.M., Davisson M.T.,	the monee underwhite gene (ww)	OCA4 ".	' . Espo ' marinana	Мау	similarity)		eyes, kidney and uterus.	ᅻ.	nearly all pigmentation in the homozygous	BLACE SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.		This SWISS-PROT entry is copyright. It is produced through a collaborat	ormatics and the EMBL outstation There are no restrictions on	as its content is in	is not removed. Usage by and for commerc	agreement (See http://www.isb-sib.ch/announ			Transmombrans. Auticon. Clusoprotoin. Wision.	increasi, drycoprocess, treaton,	CYTOPLASMIC (POTENTIAL).	ULAR (POTENTIAL).	IAL).
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	PRT	d) equen	nnota ter p	otein						ey, a	79596	ing B.)		NTS 1	74907	Hagi	, שטר	111	9 (200	feren	nelan	regra	10Cyt	are	nearl	TE SUK		righ	Or B	ions	is not	agreer	9-79	·	ye y dw	8	CYTO	EXTR	2 (PC
	STANDARD;	(Rel. 41, Created) (Rel. 41, Last seç	Rel. 41, Last an ciated transport	antigen AIM1) (Underwhite protein).	OR UW. (Mouse).			;060	N.A.	ISSUE=Eye, Kidne	MEDLINE=21372467; PubMed=11479596; Pubmachi e chimada n chima	the dene encodi	melanin content in medaka.";	Nat. Genet. 28:381-385(2001). [2]	SEQUENCE FROM N.A., AND VARIANTS UW-DBR ASN-153	MEDLINE=21473748; PubMed=11574907;	Newton J.M., Cohen-Barak O., Hagiwara	Brilliant M.H.; in the himan orthologie of	inderlie a new form of oculocutaneous	J. Hum. Genet. 69:981-988(2001).	FUNCTION: Melanocyte differentiation antigen.	s required for a	subcarature integral membrane protein; similarity)	SPECIFICITY: Melanocytes,	cts in MAT	in loss of	(: BELONGS TO TH		or entry is copy	swiss institute of Bioinic Bioinformatics Institute	non-profit institutions as long	and this statement i	entities requires a license agreement (S	edita dii emair to irodipedarab-bib.cii).	EMBL; AF360357; AAK81713.1;	MGD; MGI:2153040; Matp.		1 45		68 69
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20001	MATP_MOUSE P58355:	28-FEB-2003 28-FEB-2003	28-FEB-20 Membrane-	antigen A	MATP OR AIM1 OR UW. Mus musculus (Mouse)	Eukaryota; Metazoa;	Mammalia;	NCBI_TaxI	SEQUENCE FROM	STRAIN=dd	MEDLINE=2	"Mutation	melanin c	Nat. Gene	SEQUENCE	MEDLINE=2	Newton J.	King R.A.,	underlie	Am. J. Hu	-1- FUNCT	substances		-i- TISSUE	-1- DISEA	that results	-1- SIMILA		This SWIS	the European	À	modified	entities	מו שמונה מו	EMBL; AF3	MGD; MGI::		DOMAIN	DOMAIN	TRANSMEM
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212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 HCRARWGRRRPYILTLAIMMLLGMALYINGDAVVSALVANPROKLIWAISITWVGVVLFD 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 GSIEKVKNGGADTEQPVQEWKNKKPSGQSQRTMSMKSLLRALVNMPSHYRCLCVSHLIGW
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12 (POTENTIAL).
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                     SXTRACELLULAR (POTENTIAL)
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                           FRACELLS.
(POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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  CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                              D -> N (IN UW-DBR)
S -> P (IN UW-DBR)
                                                                                                                                                                                                                                                                                                                                Score 489.5; DB 1
Pred. No. 2.7e-28;
                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           523 YMVSAAGLGLVAIYFATQVV 542
                                                                                                                                                                                                                                                                                                         57961 MW;
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26.1%;
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                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                       530 AA;
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TRANSMEM
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SEQUENCE
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DOMAIN
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TRANSMEM
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TRANSMEM
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TRANSMEM
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RESULT 2 MATP_HUMAN

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Astraubberg R.L., Feingold E.A., Grouse i.H., Derge J.G.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Mans S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Astapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Tonshyuhi S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garrinci P., Prange C.,

Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21473748; PubMed=11574907;

Newton J.M., Cohen-Barak O., Hagiwara N., Gardner J.M., Davisson M.T.,
King R.A., Brilliant M.H. Man orthologue of the mouse underwhite gene (uw)
underlie a new form of oculocutaneous albinism, OCA4.";
Am. J. Hum. Genet. 69:981-988 (2001).

-I. FUNCTION: Melanocyte differentiation antigen. May transport
substances required for melanin biosynthesis (By similarity).
-I. SUBCELLULAR LOCATION: Integral membrane protein; melanosome (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanocytes. Defects in MATP are the cause of oculocutaneous albinism type 4 (OCA4). OCA4 is characterized by hypopigmentation of skin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9UMX9-2; Sequence=VSP_006297, VSP_006298, VSP_006299;
                                                          28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Membrane-associated transporter protein, (AIM-1 protein) (Melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=Q9UMX9-3; Sequence=VSP 006296;
TISSUE SPECIFICITY: Expressed In most melanoma cell lines and
                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                           MEDLINE=21115844; PubMed=11221837; Harada M., Li Y.F., Bl-Gamil M., Roeenbirg S.A., Robbins P.F.; Harada M., Li Y.F., Bl-Gamil M., Roeenbirg S.A., Robbins P.F.; Wige of an in vitro immunoselected tumor line to identify shared melanoma antigens recognized by HLA-A*0201-restricted T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing, Named isoforms=3;
Comment=Additional isoforms seem to exist;
Ź
530
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM AIM-1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM AIM-1B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ferro S.;
Inpublished observations (NOV-2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932;
            Q9UNX9; Q9BTM3;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq.
15-SEP-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                               Cancer Res. 61:1089-1094(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sımilarity).
ALTERNATIVE PRODUCTS:
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVĖ SPLICING.
                                                                                                                                                                                                                                                                                            TISSUE=Melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=AIM-1a;
                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=AIM-1C
                                                                                                                                                MATP OR AIM1.
                                                                                                                        antigen AIM1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPLLGSASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDPR---PLELAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 LILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCRQAYSVYAFMISLGGCLGYLLPAIDWD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
hair and eyes. It leads to reduced visual acuity.
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CAUTION: Ref.2 sequence differs from that shown due to a
frameshift in position 188.
CAUTION: The described alternatively spliced isoforms are inferred
using information from ESTs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKSFSLLRMSSKSFWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKLIMHSMAM------FGREFCYAVBAAYVTPVLLSVGLPSSLYSIVWFLSPILGFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRLLRHRKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIGPVLGLVC
                                                                                                                                                                                                                   Melanin biosynthesis; Transmembrane; Antigen; Glycoprotein; Vision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
Missing (in isoform AIM-1c).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.1%; Score 488.5; DB 1; Length 530; 26.4%; Pred. No. 3.2e-28; ive 78; Mismatches 233; Indels 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (In isoform AIM-1b).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoform AIM-1b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEGEVILOSYIGLKGLYFTGYL -> CF
                                                                                                                                                                                                                                                                                                                               4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         7 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                       3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                         1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
10 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTId=VAR 012162.
F14A4BACAA8FF31B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                               Polymorphism; Albinism; Alternative splicing.
DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                 2 (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
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EMBL; BC003597; AAH03597.1; ALT_FRAME.
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                          185 TSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPHCCPC 244
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145 TMIGVVLFDFAADFIDGPIKAYLFDVCSHQDK-EKGLHYHALFTGFGGALGYLLGAIDWA 203
                                                                                                                         204 HLELGRILGTEFOWMFFFSALVLTLCFTVHLCSISEAPL--TEVAKGI-PPOOTPODPPL
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Caryophyllidae, Caryophyllales, Chenopodiaceae, Spinacia.
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sucrose transport protein (Sucrose permease) (Sucrose-proton
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SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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InterPro: IPR005829 Sub_transporter.
InterPro: IPR005999; SuG_H_symport.
InterPro: IPR005929; Sug_transporter.
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Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,

MEDLINE=21848401; PubMed=11859360;

SEQUENCE FROM N.A. NCBI_TaxID=4896;

pombe (Fission yeast)

Schizosaccharomyces SPAC2F3.08.

g

General alpha-glucoside permease.

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237
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                                                                                        Transport; Sugar transport; Symport.
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Pfam; PF00083; sugar_tr; 1.
TIGRPAMS; TIGRO1301; GPH sucrose; 1.
SO011E; PS00116; SUGAR_TRANSPORT_1; FALSE_NEG.
PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.
                                                                                                                                                                                                                                                                          (POTENTIAL).
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es 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library.", Genes Cells 5:169-190(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctional characterization of the alpha-glucoside transporter Sut Schizosaccharomyces pombe, the first fungal homologue of plant
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of a proton (Symport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20223868; PubMed=10759889;
Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
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Transmembrane, Transport, Sugar transport, Symport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Microbiol. 39.445.454(2001).
-1- FUNCTION: Responsible for the transport of into the cell, with the concomitant export
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                                                                                                                                                                                                                                                                  ;; Score 235.5; DB 1; Length 5; Pred. No. 7.6e-10; 59; Mismatches 153; Indels
                    EXTRACELLULAR (POTENTIAL)
                                                                                                  EXTRACELLULAR (POTENTIAL)
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                                        CYTOPLASMIC (POTENTIAL).
                                                                              CYTOPLASMIC (POTENTIAL).
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
  CYTOPLASMIC (POTENTIAL).
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; Pred. No. 0.0045; |
60; Mismatches 179; Indels 126; Gaps
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                                        "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.;
                                                                                      DNA Res. 3:109-136(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 PHCCPCRARLA---------FRNLGAL--
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IIGRFAMs; TIGR00792; gph; 1.
PROSITE; PS00872; NA GALACTOSIDE SYMP; FALSE NEG
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Subcuber From N.A.

MEDLINE-21638749; PubMed=11780052;

MEDLINE-21658749; PubMed=11780052;

Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Jones M., Stavrides G., Almedda J.P., Babbage A.K., Bagguley C.L.,
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Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Danmi P.D., Dunn M.,
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
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Hurche E., Hunt A.R., Hunt S.E., Jekosech K., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., Mcconnachie L.J., Mclary R.,
Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
A Rice C.M., Ross M.T., Scott C.E., Saward C.A., Sulston J.E.,
Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.,
K. Stracey A., Tromans A.C., Vaudin M., Walli M., Wallis S.A.,
Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams L.,
Whittaker J., Willey D.L., Williams L., Williams L.,
Wanner J. Wary P.W., Hubbard T., Durbin R.M., Bentley D.R.,
Walling B. W., Hubbard T., Durbin R.M., Bentley D.R.,
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Bowden D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 414:865-871(2001).
--- PUNCTION: Pacilitative glucose transporter (By similarity).
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: Widely expressed; highest levels in liver and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
MEDIINE=21145593; PubMed=11247674;
MCVie-Wylie A.J., Lamson D.R., Chen Y.T.;
"Molecular cloning of a novel member of the GLUT family of transporters, SLC2A10 (GLUT10), localized on chromosome 20q13.1: a candidate gene for NIDDM susceptibility.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
352 RAVY-LASVAAFPVAAGATCLS-HSVAVVTASAALTGFTFSALQILPYTL 399
                                               382 KVIYFLGSMVMMGAEAGLWLVQPGQVALLYTLAIFAGVGVSVAYLIPWSM 431
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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GT10 HUMAN Sira...
28-FEB-2003 (Rel. 41, Last seque 28-FEB-2003 (Rel. 41, Last seque 28-FEB-2003 (Rel. 42, Last annot force 2003 (Rel. 43, Las
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Glucose transporter type 10)
SLC2A10 OR GLUT10.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 DC-----YGRKQAILGS-NLVLLAGSLTLGLAG------SLAWLVLGRAVV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 SASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDPRPLELALLILGVGLL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 DFCGQVCFTPLEALLSDLFRDPDHCRQAYSVYAFMISLG----GCLGYLLPAIDWDTS-- 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72; Mismatches 210; Indels 182; Gaps
          SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
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EXTRACELLULAR (POTENTIAL)
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PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.
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                                                                                                                                                                                                                                          GO; GO:0005351; F:sugar porter activity; NAS.
GO; GO:0015789; P:glucose transport; NAS.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR005829; Sug_transporter.
                                                                                                                                                                                                                  ; 606145; -. Go:0016021; C:integral to membrane; NAS
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Pred. No. 0
                                                                                                                                                    EMBL; AF321240; AAK26294.1; -.
                                                                                                                                                                EMBL, AL137188; CAB69822.2; -- EMBL; AR248053; AAK1911.1; -- EMBL; AL031055; CAA19926.2; -- Genew; HGNC.13444; SLC2A10.
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PRINTS; PR00171; SUGRTRNSPORT.
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                       TRANSPORTERS SUBFAMILY
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541 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 LSVSGIGLVSFAVPMDSGPSCL--AVPNATGQTGLPGDSGLLQDSSLPPIPRT----N 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKOVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPALCGASA 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- LLSQVAP-- 506
                                                                                                      168 FGWATAP-----AVLOSLSLLFLP--AGT---DETATHKDLIPLOGGEAPKLGPG---
                                                                ---ALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPHCCP
                                                                                                                                                                                                                                                                                                           304 VPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA---
                                                                                                                                                                                    244 CRARLAFRNIGALIPRIHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGEGLYQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 IRGRAFAFCNSFNWAANLFISLSFLDLIGTIGLSWTFLLYGLTAVLGLGFIYLF 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------SLFMG-----SIVQLSQSVTAYMVSAA-GLGLVAIY 536
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Enterobacteriaceae, Escherichia.
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Membrane topology of the pBR312 tetracycline resistance protein.
TetA-PhoA gene fusions and implications for the mechanism of TetA
membrane insertion.";
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Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tetracycline resistance protein, class A (TETA(A)).
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Nucleic Acids Res. 11:6089-6105(1983)
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MEDLINE=83299270; PubMed=6310527;
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SEQUENCE OF 85-399 FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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TIGREMS; TIGRO0880; 2 A 01 02; 1.
PROSITE; PS00216; SUGAR TRANSPORT 1; UNKNOWN 1.
Antibictic resistance; Transmembrane; Inner membrane; Transport;
Antiport; Ion transport; Hydrogen ion transport; Transposable element;
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FUNCTION: RESISTANCE TO TETRACYCLINE BY AN ACTIVE TETRACYCLINE BFFLOX. THIS IS AN ENERGY DEPENDENT PROCESS THAT DECREASES THE ACCUMULATION OF THE ANTIBLOTIC IN WHOLE CELLS. THIS PROTEIN FUNCTIONS AS A METAL-TETRACYCLINE/H+ ANTIPORTER. SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane SIMILARILY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY.
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M -> V (IN REF. 3).
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InterPro, IPR007114; MFS..
InterPro, IPR005828, Sub_transporter.
InterPro, IPR005829; Sug_transporter.
InterPro, IPR001958; TCR_TetA.
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72 GSASDHWRGRYGRR	139 CFGFGWVAGPVLGGLM	283MALMIFILFYIDFVGBGLYQGVPRAEPGTEARRHYDBGVRMGSLGLFLQCAI : : :	335 SLVFSLVMDRLVQRFGTRAVYLASVAAFPVAAGATCLSHSVAVVTASÄALTGFTF 389 :::	390 SALQILPYTLASLYHREKQVFLPKYRGDTGGASSEDSLMTSFLPGP 435	RESULT 8 PURB STRLP TD FURB STRLP AC P42670; DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1995 (Rel. 32, Isat sequence update) DT 01-NOV-1095 (Rel. 32, Isat sequence update)		Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces. NCBI_TaxID=132472;	- (0 (0 -	Tercero J.A., Lace "The pur8 gene fro	puro Eur.	1	ENVIRONMENT. -!- SUBCELLULAR LOCATION: Integral membrane protein. -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY.)	This		modified and this statement is not removed, entities requires a license agreement (See		A InterPro; IPR004638; Efflux EmrB. A InterPro; IPR007114; MFS. A InterPro; IPR005828; Sub_transporter.
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larity 23.2%; Pred. No. 0.13;
Conservative 61; Mismatches 175; Indels 197; Gaps
                                                     83; sugar tr; ].
1006; TCRTERS.
1GROJ1: efflux EmrB; 1.
resistance; Antibiotic biosynthesis; Transmembrane;
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367 POTENTIAL.
371 EXTRACELLULAR (POTENTIAL).
392 CYTOPLASMIC (POTENTIAL).
443 POTENTIAL.
461 EXTRACELLULAR (POTENTIAL).
461 EXTRACELLULAR (POTENTIAL).
482 POTENTIAL.
503 CYTOPLASMIC (POTENTIAL).
503 CYTOPLASMIC (POTENTIAL).
51852 MW; FA3B814DF9A3EB74 CRC64;
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PR001411; TCR_TetB.
83; sugar_tr; 1.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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MEDLINE-21074935; PubMed=11206551;
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
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                                                 515 QLSQSVTAYMVSAAGLGLVAIYFA 538
                                                                   AmpG protein.
AMPG OR B0433 OR Z0536 OR ECS0487.
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                Kuhara S., Shiba T., Hattori M., Shinagawa H.;
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-1- FUNCTION: PROBABLY ACTS AS A PERMEASE IN THE BETA-LACTAWASE
INDUCTION SYSTEM AND IN PEPTIDOGLYCAN RECYCLING.
-1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.2%; Score 119.5; DB 1; Length 491;
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G -> D (TN ...
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InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporte:
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TIGRFAM8; TIGR00901; ZA0125; 1.
Transport; Transmembrane; Inner
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AP002551; BAB33910.1;
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Matches 126; Conservative
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PIR; S37391; S37391.
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151
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53 MTMVLGIGPVLGLVCVPLLGSASDHWRGRYGRRRPFIWALSLGILLSLFLI-PRAGWLAG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 ----SGNPILVPAFLLIGELSLMG----LTFGPMGALLPELF--PTEVR--YTGASFSYNV 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SETRALNE-IT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534949 bubMed=11677609;
MCDLINE-21534949 M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hongo E., Morimyo M., Mita K., Machida 'I., Hama-Inaba H., Tsuji H., Ichimura E., Noda Y.; "The methyl viologen-resistance-encoding gene smvA of Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Hypothetical protein; Transport; Transmembrane; Inner membrane;
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CYTOPLASMIC (POTENTIAL)
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Methyl viologen resistance protein smvA.
Salmonella typhimurium.
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NCBI_TaxID=602;
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384
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410
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Best Local Similarity
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SMVA_SALTY
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                                                                                                                 -----TIP-----VPKTLEOAVVAPLRDFFGRN 222
                                                                                                                                                                                                                                223 NAWLILLIVLYKLGDAFAMSLTTTFLIRGV-----GFDAG----EVGVVNKTLGLLATIV 274
                                                                                                                                                                                                                                                                                                                                                                                                                453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 LLSITDKHLYSMGAAVFFENLCGGMGTSAFVALLMT-------LCNKSFSATQFAL 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511 GSIVQLSQ-----SVTAYMVS-----AAGLGLVAIYFATQVVFDKSDLAKYS 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 LLVCRQTLEYTRVNDNFISRTAYPAGYARAMWTLAAGUSLLAVWLLL-LIMDALDLTHFS 457
     MLVSGGLALWL--ADKW------LGWOG--MYWLMAALLIPCIIATLLAPE----PT 198
                                                                                                                                                                             280 CSWMALMTFTL----FYTDFVGEGLYQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCA 333
                                                                                                                                                                                                                                                                                               334 ISLVFSLVMDRLVQRFGTRAVYLASVAAFPVAAGATCLSHSVAVVTASAALTGFTFSALQ 393
                                                                                                                                                                                                                                                                                                                                                        275 GALYGGILMORLSL---FRALLIFGI---------LQGASNAGYW 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12 / MG1655;
MEDLINE=94316500; Pubmed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
Fanalysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                             ILPYTLASLYHREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL
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-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. STRONG, TO
H.INFLUENZAE H10281 AND H10418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                              227 EPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAEL-
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PIR; S47743; S47743.
ECGGENE; EG12249; yhl8.
ECGGENE; EG12249; yhl8.
INTERPO: IPR007114; MFS.
INTERPO: IPR007114; MFS.
INTERPO: IPR005829; Sub_transporter.
INTERPO: IPR005829; Sug_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGRFAMB; TICR00883; 2A0166; 1.
PROSITE; PS00217; SUGAR_TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT 2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Hypotherical metabolite transport protein yhjB.
YHJE OR B3523.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                          'Complete genome sequence of Salmonella enterica serovar Typhimurium
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                              Nature 413:852-856(2001).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
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21.0%; Pred. No. 0.27;
ive 60; Mismatches 151; Indels 136;
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961F77C748CDA164 CRC64;
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Y (IN REF. 1).
Y (IN REF. 1).
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InterPro; IPR001411; TCR TetB.
PRINTS; PR01036; TCRTETB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inner membrane;
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EMBL; AE008769; AAL20492.1;
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211 VAATLLVAEEAALGPTEPAE-GLSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPR 269
                                                                      365 -AASALLASTSAIMAAAPAEKAAAAGAIETMAYELGAGLGIAIFGLLLSRSFSASIRLPA 423
                                                                                                                                                    270 TLRRLFVAELCSWMALMTFTLFYTDFVGEG--LYQGVP--RAEPGTEARRH---YDEGVR 322
                                                                                                                                                                                                                      424 GLEAQEIARASSSM------GEAVQLANSLPPTQGQAILDAARHAFIWSHSVA 470
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STRAIN=CDC 1551 / Oshkosh;
Fleiscohmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleiscohmann R.D., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H, Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Daviss R., Devlin K., Feltwell T., Geneles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Patiphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Mcure 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: TO POLYPEPTIDE 5 OF THE NADH-UBIQUINOL OXIDOREDUCTASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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01-0CT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-2003 (Rel. 41, Last annotation update)
Hypothetical protein Rv0083.
RV0083 OR MT0090 OR MTCX251.01 OR MTV030.27.
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InterPro; IPR001750; Oxidored_q1.
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PRINTS; PR01437; NUOXDRDTASE4
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Tuberculist; Rv0083;
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Propionibacterineae; Nocardioidaceae; Nocardioides.
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                                                                                                                                                                                                                                         93 AAMLLVPAAGSVTTFLLAWELMAIASLILVLSEHARPQVRSAGLWYAVMTQLGFIAILVG 152
                                                                                                                                                                                                                                                             -------EIPRAGWLAGL 112
                                                                                                                                                                                                                                                                              LVVLAAAG-GSDRFAG-----LGAVCDGVRAAVFMLTLVGFGSKAGLVPLHAWLPRA 203
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                                                                                                                                                                                                                                                                                                                      246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPKPGAPFPNGHVGAGGSGLLP-----PPPPA----LCGASACDVSVRVVVGEPTEAR 481
                                                                                                                                                                                                                                                                                                              204 HPEAPSPVSALMSAAMVNLGIYGIVRFDLQL-----LGPGPRWWGLA----L
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                                                                                                                                                                                3.9%; Score 111.5; DB 1; Length 640;
22.3%; Pred. No. 0.87;
ive 73; Mismatches 222; Indels 155;
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                                                                                                                                                               6254C289DBD108A8 CRC64;
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          protein; Oxidoreductase; Transmembrane;
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15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Probable 1-hydroxy-2-naphthoate transporter. Nocardioides sp. (strain KP7). Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;

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tive 66; Mismatches 180; Indels 110; Gaps
                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                    Iwabuchi T., Harayama S.;
"Biochemical and genetic characterization of 2-carboxybenzaldehyde dehydrogenase, an enzyme involved in phenanthrene degradation by Nocardioides sp. strain KP7.";
J. Bacteriol. 179:6488-6494(1997).
-I. FUNCTION: PROBABLY INVOLVED IN THE TRANSPORT OF 1-HYDROXY-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.9%; Score 111; DB 1; Length 473; 24.3%; Pred. No. 0.69;
                                                                                                                                                                                                              (Potential).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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D6D765D376260D8A CRC64;
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EXTRACELLULAR (POTENTIAL)
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InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
SEQUENCE FROM N.A.
MEDLINE=97474276; PubMed=9335300;
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FGL----GAVMPVAL-TIVADWM--PKARRAQMVSIAFAGVGVGSIIGAYLAA-----A 172
                                         VIPTLĠWQVMVLIAĠLAPLIILPPFVA--LVPEPAIISVRRGIPEARIRSALALVAPDRD 230
                                                                                                                            GVFFVVQGSGLLVLQYMPMLLQAPAPGLST---VESGLIVAMYGWG-----ALIGQLTIA 322
                                                                                                                                                344 RIVORFGTRAVYLASVAAFPVAAGATCLSHSVAVVTASAALTGFTF-----SALQI-L 395
                                                                                                                                                                    323 FILKRF-DRFIALAAFIFWSV------VGLLIVAAFGTGFGFFFGYFTLLFAIGLSL 371
                       ALGPTEPAEG
                                                              LSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLF
                                                                                                        YTDFVGEG----LYQGVP----RAEPGTEARHYDEGVRMGSLGLFLQCAISLVFSLVMD
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=92109659; PubMed=1764025;
Thomas J.T., Cresswell C.J., Rash B., Nicolai H., Jones T.,
Solomon E., Grant M.E., Boot-Handford R.P.;
"The human collagen X gene Complete primary translated sequence and chromosomal localization.";
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Reichenberger E., Beier F., Luvalle P., Olsen B.R., von der Mark K.,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE OF 561-666 FROM N.A.
MEDLINE=91243838; PubMed=2037056;
Apte S., Mattei M.-G., Olsen B.R.;
"Cloning of human alpha 1(X) collagen DNA and localization c
COL10Al gene to the q21-q22 region of human chromosome 6.";
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Apte S.S., Seldin M.F., Hayashi M., Olsen B.R.;
Cloning of the human and mouse type X collagen genes and the mouse type X collagen gene to chromosome 10.";
Eur. J. Blochem. 206:217-224(1992).
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Beier F., Lammi M.B., von der Mark K.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                      (Rel. 32, Created)
(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                    STANDARD;
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"Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
associated collagen (type IX), and network-forming collagen (type X)
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                                                               SEQUENCE OF 547-655 FROM N.A.
MEDLINE-92077285; PubMed-1743401;
Reichenberger E., Aigner T., von der Mark K., Stoeb H., Bertling W.;
"In situ hybridization studies on the expression of type X collagen in fetal human cartilage."
In fetal human cartilage.
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MEDLINE=95181449; PubMed=7876225;
Chan D., Cole W.G., Rogers J.G., Bateman J.F.;
"Type X collagen multimer assembly in vitro is prevented by a Gly
to Val mutation in the alpha 1(X) NCI domain resulting in Schmid
metaphyseal chondrodysplasia.";
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MEDLINE=94272470; PubMed=8004099;

McIntCosh I., Abbott M.H., Warman M.L., Olsen BiR., Francomano C. "Additional mutations of type X collagen confirm COL10A1 as the Schmid metaphyseal chondrodysplasia locus.";

Hum. Mol. Genet. 3:303-307(1994).
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REVIEW ON VARIANTS.
MEDLINE=97255959; PubMed=9101290;
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Lett. 282:393-396(1991).
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MEDLINE=99057503; Pub
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                                                              MEDLINE=99069781; PubMed=9852679;
Sawai H., Ida A., Nakata Y., Koyama K.;
Sawai H., Ida A., Nakata Y., Koyama K.;
Toysteine at codon 597 of the type X collagen gene associated with resulting in the substitution of tyrosine by the cysteine at codon 597 of the type X collagen gene associated with schmid metaphyseal chondrodysplasia.";
Thum. Genet. 43.559-56,[1998].
The chondron are the third position of the tripeptide repeating to the third position of the tripeptide repeating to the chains.
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Extracellular matrix; Connective tissue; Repeat; Hydroxylatic
Cartilage; Collagen; Signal; Disease mutation; Polymorphism;
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NONHELICAL REGION (NC1).
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GO; GO:0005202; F:collagen; TAS.
GO; GO:0001501; P:skeletal development; TAS.
InterPro; IPR001073; C1q.
InterPro; IPR001073; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF00391; Collagen; 8.
PRINTS; PR00007; COMPLEMNTC1Q.
SWART; SM00110; C1Q; 1.
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J. Hum. Genet. 63:1659-1662(1998).
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EMBL; S68531; AAC60615.1; --
EMBL; X58879; CAA41686.1; --
EMBL; M74050; AAA61221.1; --
EMBL; X72579; CAA51170.1; --
EMBL; X72580; CAA51170.1; --
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PDB; IGR3; 14-FEB-02.
Genew; HGNC:2185; COLIOA1.
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                                                                                                                                                                                                               463 PGSKGDPGSPGPPGPAGIATKGLNGPTGPPGPPGPRGHSGEPG---LPGPP-----
                                                                                                                                                                                                                                              468 VSVRVVVGEPTEARVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSA
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liamma T.P., Pathi Z., Hort Y.J., Iben L.G., Dutton J.L., Baker E.,
Sutherland G.R., Shine J.,
"Structural organization and chromosomal localization of three human
                                                                                                                                                35; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                  DB 1; Length 680;
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Smith K.E., Walker M.W., Artymyshyn R., Bard J., Borowsky B.
Tamm J.A., Yao W.-J., Vaysse P.J.-J., Branchek T.A., Gerald
                                                                                                                                               11; Mismatches 51; Indels
                              G -> R.
/FTIG=VAR 001840.
C -> R (IN SMCD).
/FTIG=VAR 001841.
G -> R (IN SMCD).
/FTIG=VAR_001839.
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Pred. No. 1.1;
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Ann. N.Y. Acad. Sci. 863:56-63(1998).
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MEDLINE=99048961; PubMed=9832121;
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J. Neurochem. 71:2239-2251(1998).
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                                                                                                                   3.9%;
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         MEDLINES FORCH N.A.

RAD BUDDAN I. RULL A.R. COLIDING J.E. BRUSAKIEWICH R., Beare D.M.,
Cland M., Smink L.J., Alinecough R., Almeda J.D., Babbage A.K.,
Cland M., Smink L.J., Colling J.E., Barcek K.N., Beasley O.P.,
RA Bagguley C., Balkey S.E. Bridgeman A.M., Buck D., Burgess O. P.,
RA GLOGY V. Blakey S.E. Bridgeman A.M., Buck D., Burgess O. P.,
RA DHAMIN D. Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
Clegg S.M., Cobly N.E., Coville G.J., Outbin R.M., Ellington A.G.,
RA DHAMI P.D., Dockree C., Dodworth S.J., Dutbin R.M., Ellington A.G.,
RA SILE E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA HURL S.E., Jones M.C., Kershaw J., Kinherley A.M., King A.,
RALL R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Mortmore B.J.,
RAD R.E., Johnson M.C., Kershaw J., Kinherley A.M., King A.,
RAD RAD R.E., Johnson S., Medulturay A.A., Milne S.A., Mortmore B.J.,
RAD RAD R. B. Johnson S., Medulturay A.A., Milne S.A., Mortmore B.J.,
ROCIE C.E., Sehra H.K., Skuce C.D., Smith M.L.,
RAD RAD R. B. Burd R. W., Skuce C.D., Smith M.L.,
RAD R. Soderlund C., Spragon L., Steward C.A., Sulscon D., Phillimore B.J.,
RAD WIlliams S.A., Williams S.A., Williams S.A., Milliams D., Williams D., Williams S.A., Milliams S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0007611; P:learning and/or memory; TAS.
GO:0007194; P:negative regulation of adenylate cyclase ac.
GO:0007218; P:neuropeptide signaling pathway; TAS.
GO:0007268; P:synaptic transmission; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0005886; C:plasma membrane; TAS.
GO:0004966; F:galanin receptor activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0016021; C:integral to membrane; TAS.
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GO; GO:0004966; F:galanin receptor
GO; GO:0007631; P:feeding behavior;
GO; GO:0007631; P:learning and/or
GO; GO:0007194; P:negative regulation
GO; GO:0007288; P:neuropeptide sign
GO; GO:0007288; P:syraptic transmis
InterPro; IPR000276; GPCR_Rhodpsn.
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EMBL; AF129514; AAD47348.2; -.
EMBL; AF129513; AAD47348.2; JOINED.
EMBL; Z97630; -; NOT ANNOTATED_CDS.
Genew; HGNC:4134; GĀĒR3.
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21.9%; Pred. No. 0.63;
iive 35; Mismatches 145; Indels 156; Gaps
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PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS002437; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                             G-protein coupled receptor; Transmembrane, Multigene family; Lipoprotein; Palmitate.

DOMAIN 21 41 1 PANNSMEM 21 41
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TISSUE=Prostate;

MEDLINE=21139094; PubMed=11245466;

MEDLINE=21139094; PubMed=11245466;

MEDLINE=21139094; PubMed=11245466;

Filho A.M., Nolasco M., Badaro R., Reed S.G.;

"Identification and characterization of prostein, a novel prostate-specific protein.";

Seconcer Res. 61:1563-1568(2001).

EMBL, AV033593; AAK54386.1; -.

SEQUENCE 553 AA; 59322 MW; OAFA23FBC742A667 CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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181 IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPAEGAESAPSLPSH
                                                        CCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGEGL
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last sequenc
01-MR-2003 (TrEMBLrel. 23, Last annotat
Hypothetical protein (PROSTEIN homolog)
2210413P12RIK.
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553 AA; 59
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Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypotherical 59.4 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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Submirted (Apr-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB060851; BAB46871.1; -.
Hypothetical protein.
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98.2%; Pred. No. 1.6e-204;
iive 2; Mismatches 8;
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TDFVGEGLYQGVPRAELGTEARRHYDEGVRMGSLGLFLQCAISLVVDRLVQRFGTR
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                                                                   SAPSLPSHCCPCWARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLFY
                                                                                                                                   TDFVGEGLYQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTR
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                                            SAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLFY
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01-057-2002 (TrEMBLrel. 22, Last sequence update)
01-067-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4 prothetical protein (Fragment).
2210413P12RIK.
Mus musculus (Mouse).
Mus musculus (Mouse).
Musmalia; Metazoa; Chordata; Craniata; Vertebrata; El Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; P. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.4%; Score 2099; DB 11; Best Local Similarity 90.0%; Pred. No. 1.7e-151; Matches 404; Conservative 12; Mismatches 33;
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Submitted (JUL-2002).to the EMBL/GenBank/DDBJ
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MGD; MGI:1922082; 2210413P12Rik.
InterPro; IPR005805; Rieske.
PROSITE; PS00200; RIESKE_2; 1.
Hypothetical protein.
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                                              YQGVPRAEPGTEARRHYDEGIRMGSLGLFLQCAISLVFSLVMDRLVQKFGTRSVYLASVM 360
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                                                                                                           IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH 240
                                                                                                                                CCPCHVGLAFRNLGTLFPRLQQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGEGL 300
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TISSUB-Medulla oblongata;
TISSUB-Medulla oblongata;
TISSUB-Medulla M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypotherical 53.4 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 501 AA; 53447 MW; 8C554BBD04EE0470 CRC64;
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VVFDKNDLAKYS 552
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01-JUN-2002 (TrEMBLrel. 21, Created)
   FlyBase; FBgn0035968; CG4484.
SEQUENCE 599 AA; 66057 MW;
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Submitted (MAR-2002) to the
EMBL; BC024519; AAH24519.1;
Hypothetical protein.
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RA Adams M.D., Celniker S.E., Holt R.A., Bands R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Abburner M., Henderson S.N.,
RA George R.G., Scherer S.E., Richards S., Abburner M., Henderson S.N.,
RA George R.G., Worten J.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Fériffer B.D.,
RA Ballaw R.M., Baud A., Baxendale J., Bayraktarold L., Beasley B.M.,
RA Ballaw R.M., Baud A., Barenan B.P., Bhandari D., Blobhakov S.,
RA Burtis R.C., Busam D.A., Burler H., Cadleu B., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Burler H., Cadleu B., Davies P.,
RA Burtis R.C., Cabriellan R.E., Davies P., Brother P., Brother P.,
RA Burtis R.C., Gabriellan A.E., Garty R.A., Chandra I.,
RA Burtis R.C., Gabriellan A.E., Garty R.A., Changer C., Ferriera S., Pleischmann W.,
RA Burtis R.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gubar W., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush P., Karpen G.H., Ke Z., Kunison J.A., Ketchum K.A.,
Alalai M., Kalush P., Karpen G.H., Ke Z., Kunison J.A., Ketchum K.A.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mornt S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Minal B.E., Kodira C.D., Kraft C., Kratik C., Kratik C., Rocheler F., Shen H.,
Shue B.C., Siden-Kamos I., Simpson M., Stupsk M.P., Rang X.,
Rang Z.-Y., Massarman D.A., Waisherco M., Wang X.,
Rang Z.-Y., Wassarman D.A., Waisherco M., Wang X.,
Rang Z.-Y., Wassarman D.A., Waisherco M., Wang X.,
Rang Z.-Y., Wassarman D.A., Waisherco M., Yang S., Zhon Q., Xang S., Zhon M., Zhong F.W., Zhong F.W., Zhong F.W., Zhong W., Zhong W.
                                                      463
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HREKQVFLPKYRGDAGGSSGEDSQTTSFLPGPKPGALFPNGHVGSGSSGILAPPPALCGA
                                                                                                                        SACDVSVRVVVGEPTEARVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAY
                                                                                                                                                      361 SACDVSMRVVVGEPPEARVVTGRGICLDLAILDSAFILSQVAPSLFMGSIVQLSHSVTAY
                                                     HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPALCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Last annotation update)
                                                                                                                                                                                         MVSAAGLGLVAIYFATQVVPDKSDLAKYS 552
                                                                                                                                                                                                             MYSAAGLGLVAIYFATOVVFDKNDLAKYS 449
                                                                                                                                                                                                                                                                                                              599
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NCBI_TaxID=7227;
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MEDLINE=20196,006; PubMed=10731132;
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EMBL; AE003552; AAF50310.1;
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CG4484.
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                                                                                                                                                                                                                                                                                                                                                                                     106 AGWLAGLLC-----PDPRPLELA--LLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHC 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 RQAYSVYAFMISLGGCLGYLLPAIDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 QILPYTLASLYHREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                          183;
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C5381D334CFBF2EB CRC64;
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Last annotation update)
                                                Query Match 18.2%; Score 519.5; DB 5; Best Local Similarity 23.7%; Pred. No. 2.7e-31; Matches 150; Conservative 100; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 MGSIVQLSQSVTAYMVSAAGLGLVAIYFATQVVF
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01-JUN-2002 (TrEMBLrel. 21, Last annotat
Hypothetical 11.4 kDa protein (Fragment)
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	NUT 9 2274 290274 PRELIMINARY; Q90274; Q1-DEC-2001 (TrEMBLrel. 19, C 01-DEC-2001 (TrEMBLrel. 19, L 01-OCT-2002 (TrEMBLrel. 22, L Membrane-associated transport		RX SIXALINE=N11; RX FUKAmachi S., Shimada A., Shima A.; RT "Mutations in the gene encoding B, a novel tran RT melanin content in medaka."; RI Nat. Genet. 28:381-385(2001). DR EMBL; AF332510; AAK77024.1; SQ SEQUENCE 576 AA; 63411 MW; 13A5C9828ABEE894 Query Match 15.9%; Score 456; DB 13;	Heer Local Similarity 24.0%; Pred. No. Matches 144; Conservative 95; Mismat 12 RHRKAQLLLVNLLTFGLEVCLAAGITYVP :: : ::	8 & f	116 GSASDYCRSSWGRRRPYILVLGILMLVGLSWFLNDI 133 QY 115 PDPRPLELALLILGVGLLDFCGQVCFTPLEALLSDL- 153 Db 168AIVVVMFGVVLFDFAADFIDGPIKAYLFDVCS	Oy 173 CLGYI Db 219 ACGYI	244 Qy 212 -AATLLVAEEAALGPTEPAEGLSAPSLSPHCC	245	297 GEGLYGGVPRAEPGTEARRHY 19	357
0; Gaps ALLDSAFLL ALLDSAFLL	SQVAPSLFMGSIVQLSQSVTAYMVSAAGIGLVAIYFATQVVFDKSDLAKYS 552	23, Created) 23, Last sequence 23, Last annotati 1sporter protein. rdata, Craniata, V	PubMed=12466851; tium, Exploration Research Group Phas mouse transcriptome based on fu 1 (2002). AC41003.1;	4268989/3H/D642U CKC64; GCore 484.5; DB 11; Length 530; Pred. No. 1.1e-28; ; Mismatches 229; Indels 101; Gaps	17 QLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIGPVLGLVCVPLLGSASD 76	77 HWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDPRPLELALLILGVGLLD 13 	GCLGYLLPAIDWDTSALAPYLG 	LIFTICVAATLLVAREAALGFUEPAEGLGAPSLSPHCCPC :: VIICEITHLCSIPEAFLRDAATDPPSQQDPQGSSLSASGMHEY		MALMIFTLFXTDFVGEGLYQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVM 34 :: : : : :	DRLVQRFGTRAVYLASVAAFPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASL 40

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17;
LPRSLYSLVWLISPILGFLLQPII 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --FRDPDHCRQAYSVYAFMISLGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----IPRAGWLAGLLC 114
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FLIVHLFSIPEKPLAKVPSESSA 278
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6;
98; Indels 164; Gaps
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ebrata; Euteleostomi;
leostei; Neoteleostei;
Atherinomorpha;
ryzias.
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	CLDIAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQVVF 543	SEQUENCE FROM N.A. STRAIN=AX4; Gloeckner G., Eichinger L., Szafranski K., Pache Gloeckner G., Eichinger L., Szafranski K., Pache Lehmann R., Baumgart C., Parra G., April J.F., G Tunggal B., Cox E., Quail M.A., Platzer M., Rose "Sequence and Analysis of Chromosome 2 of Dictyc Submitted (MAY-2002) to the EMBL/GenBank/DDBJ da-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROT EMBL, AC117076, AAM33692.1; InterPro; IPR005828; Sub_transporter. Fransmomptane. Transmembrane.	SQ SEQUENCE 754 AA; 82774 MW; 614C473C932ACCE4 CRC64; Query Match Best Local Similarity 23.5%; Pred. No. 1.1e-21; Matches 128; Conservative 90; Mismatches 200; Indels 127; Gaps 13; Qy 13 HRKAQLLLVNLIFFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIGBVLGLVCV 68 : : : : :		187 ARMYPERILIGIOECULIGIES IN CONTINUE IN THE STATE OF TH	KARFGEAKKINDEGVINGSLOLFLUCALSDYSLUVINGLYKETOKAYILASYANFEYA :: :
477 PT 532 537 F	RESULT 10 Q8K4S3 ID Q8K4S3 FOI-2002 (TrEMBLrel. 22, Created) DT 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) DT 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) DT 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) DT 01-0CT-2002 (TrEMBLrel. 22, Last annotation update) DT 01-MED TAIL TREMBLREL. 22, Last sequence update) DR Proton-associated sugar transporter A. GN Rattus norvegicus (Rat). OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. CX NCBL TaxID=10116; RN [1] RP SEQUENCE FROM N.A.	RA Shimokawa N., Okada J., Haglund K., Dikic I., Koibuchi N., Miura M.; RT "Past-A, a new class proton-associated sugar transport facilitator in RT the central nervous system."; RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL; AB075229; BAB97313.1; KW Sugar transport. SQ SEQUENCE 751 AA; 81751 MW; 5C33E1C2E4A1B2EC CRC64; Query Match	Qy 17 QLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFWTWVLGIGPVLGLVCVPLLGSASD 76	205 FSADSADNPSHAYMADVCGPVDQDR-GLANIHALMAGLGGGGFGYVVGGIHWDKTSFGRALG 194 TQEECLFGLLTLIFLTCVAATLLVA		442 SLDTSKPRASGILKRPQTLALPDVAGGNGPETSKRRNVTFSQQVANILLNGVKYESELIG 260LHQLCCRMPRILRRLFVAELCSWMALMTFTLFYTDFVGEGLYQGVPR

Db 356 GAGFVW	PRELIMINARY; 000 (TrEMBLrel. 13, Le 003 (TrEMBLrel. 23, Le 103 (TrEMBLrel. 23, Le transporter protein. arota (Carrot). a; Viridiplantae; Stre phyta; Magnoliophyta; phyta; Magnoliophyta; phyta; Magnoliophyta; rROM N.A. oot; ID=4039; ID=40301; ID=4039; ID=4039;	Ouery Match 12.1%; Score 346.5; DB 10; Length 515; Best Local Similarity 27.2%; Pred. No. 3.2e-18; Matches 137; Conservative 76; Mismatches 215; Indels 75; Gaps 19; 17 QLLLVNLTFGLEVCLAAGITYVPPLLLEVGVEKFWTWVLGIGPVLGVVPLLGSASD 76 18 St.VLVAAIAAGVQFGMALQLSLLTPYQLLGIPHKWAAYIMLGGPIGGVLGVVPLLGSASD 76 19 KLVLVAAIAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
359 VAAFPVAAGATCLSHSVAVVTASAALTGFTFSALQIL 395	K6 PRELIMINARY; PRT; 501 AA. K6; AY-2000 (TrEMBLrel. 13, Created) AY-2000 (TrEMBLrel. 13, Last sequence update) AR-2003 (TrEMBLrel. 23, Last annotation update) AR-2003 (TrEMBLrel. 23, Last annotation update) AR-2003 (TrEMBLrel. 23, Last annotation update) AR-2004 (TrEMBLrel. 23, Last annotation update) C11. C11. C12. C13. C14. C14. C15. C15. C15. C16. C17. C17. C18. C18. C18. C18. C18. C18. C19. C19. C19. C19. C19. C19. C19. C19	12.1%; Score 346.5; DB 10; Length 501; Best Local Similarity 27.0%; Pred. No. 3.18-18; Indels 133; Gaps 22; Best Local Similarity 27.0%; Pred. No. 3.18-18; Indels 133; Gaps 22; Matches 153; Conservative 83; Mismatches 197; Indels 133; Gaps 22; Qy

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS1/gcgdata/geneseg/geneseg-emb1/AA2000.DAT; /SIDS1/gcgdata/geneseg/genesegy-emb1/AA2001.DAT; /SIDS1/gcgdata/geneseg/genesegy-emb1/AA2002.DAT; /SIDS1/gcgdata/geneseg/genesegy-emb1/AA2003.DAT;

/SIDS1/gcgdata/geneseq/geneseqp-embl

SUMMARIES	h DB ID Description	19	19 AAW69385	21 AAB28527	21 AAY82002	22 AAU69763	22 AAU04961		כטטססטעע ככ
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Prostate tumour an	Human prostate tum	Prostate tumour pr		8		Human PROST 03. H		Prostate cancer sp	Prostate tumour an	Prostate specific	Thioredoxin-ubiqui	Alpha prepro-P501S	Human prostate spe		Human prostate cDN	P553S splice varia	-	_	Human P553S splice	Prostate cancer as	Human prostate pro	O	Ra12-P501S-E2 cons	Prostate cancer as	Protein encoded by	Human prostate-rel	Prostate-specific	Human prostate-spe	Amino acid sequenc	Human mast cell re	Human secreted pro	prostate	P553S splice varia	Human P553S splice	Prostate cancer as
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AB74800	41	76665	57	ABG61900	ABB95222	AAU10324	AAU82643	ABU71653	AAB74830	ABU71860	AAM50661	AAM01318	ABU71887	AAM50662	AAU69875	AAM01230	AAE01362	ABG64105	ABB95335	ABU71766	AAU69907	AAM01262	ABB95367	ABU71798	AAW85068	AAB29268	AAU04205	AA019084	54369	77571	AAE01423	AAU69873	22	m	71764
AAB	ABG	ABG76	ABB77	ABG	ABB	AAU	AAU	ABU	A B	ABU	AAM	AAM	ABU	AAM	AAU	AAM	AAE	ABG	ABB	ABU	AAU	AAM	ABB	ABU.	AAM	AAB	AAU	AAO	AAY54	ABB77	AAE	AAU	AAM01	ABB95	ABU71
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	Protein; 553 AA	
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	standard;	
	LT 1 1869 AAW71869	AAW71869

RESULT 1 AAW71869

ALIGNMENTS

Prostate; cancer; tumour; vaccine; immunogen; clone Amino acid encoded by prostate tumour clone L1-12. 98US-0020956. 97US-0806099. 97US-0904804. 98WO-US03492. 09-FEB-1998; 25-FEB-1997; 01-AUG-1997; Homo sapiens. WO9837093-A2. 25-FEB-1998; 06-JAN-1999 27-AUG-1998

WPI; 1998-609886/51. N-PSDB; AAV61201. Dillon DC, Xu J;

(CORI-) CORIXA CORP.

Polypeptides comprising immunogenic portions of prostate proteins

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481 RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ 540
         WO9837418-A2
                             27-AUG-1998
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                              The present sequence is an immunogenic portion of a prostate tumour protein. The immunogen, or the DNA encoding it, can be used as a vaccine for the treatment of prostate cancer. The immunogen was isolated from a prostate tumour cDNA library obtained by subtracting a prostate tumour cDNA library with a normal tissue cDNA library.
                                                                                                                                                   Gaps
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                                                                                                                               Length 553;
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 a vaccine for the treatment of prostate cancer
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                                                                                                                            Query Match 100.0%; Score 553; I Best Local Similarity 100.0%; Pred. No. 0; Matches 553; Conservative 0; Mismatches
                  Page 82-84; 130pp; English
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08-DEC-1998
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This sequence is encoded by a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as this protein sequence). An antibody which binds to an immunogenic prostate protein, which binds to an immunogenic monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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                                                                                                                                                                                                                                                                                                                                                                          Novel human prostate specific tumour protein and fragments for detecting and treating prostate cancers
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97US-0904809.
98US-0020747.
98WO-US03690
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nes 553; Conservative
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N-PSDB; AAV58586.
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25-FEB-1998;
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01-AUG-1997;
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The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express
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                                                                                         YOGVPRAEPGTEARRHYDEGVRMGSLGLFLOCAISLVFSLVMDRLVQRFGTRAVYLASVA
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                                                                                                                                           361 AFPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG
                                        CCPCRARLAFRNLGALLPRLHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; diagnosis; tumour; gene therapy; detection; immunogenic; cytostatic; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aptide useful for treating and diagnosing an immunogenic portion of prostate tumor
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98US-0116134.
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15-JAN-1999;
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14-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is encoded by a cDNA sequence which was isolated from a breast tumour CDNA library. It is provided in a specification relating to compounds for immunotherapy and diagnosis of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to produce a vaccine.
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                                                                                                                                                                                                                                 Human; breast tumour antigen; cytostatic; immunotherapy;
                                                                                                                                                                                                        Protein encoded by human breast tumour cDNA clone P501S.
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity 100.
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                                       WFDKSDLAKYSA
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the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prosette cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of reh polymuclectides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06241 to AAA06591 and AAX82000 to AAX82020 represent sequences used in the exemplification of
                                                                                                                                                                                                                                        9
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100.0%; Pred. No. 0;
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derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polymucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polymucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The Oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
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Carter
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A, Day CH, Vedvick TS,
epler WT, Henderson RA;
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100.0%; Pred. No., 0;
ive 0; Mismatches
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GR, Retter MW, Stolk JA, Day C
Wang A, Skeiky YAW, Hepler WT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide of the invention.
                                                                                                                                 2000US-0651236.
2000US-0657279.
2000US-0679426.
2000US-0685166.
                                                          2000US-0568100
2000US-0570737
                                                                                                     2000US-0605783
2000US-0636215
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                                                                                      13-JUN-2000;
27-JUN-2000;
10-AUG-2000;
               27-MAR-2001;
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Kalos MD, Fanger GR,
Wang A, Meagher MJ;
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RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ
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100.0%; Pred. No. 0;
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Best Local Similarity 100.
Matches 553; Conservative
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(I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies of (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93157 to AAH93944 and AAM01115 to AAM01318 represent polymucleotide and amino acid sequences used in the exemplification of the present invention.
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The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have eytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. In agenomic region on chromosome 224112, P704P, P75P and B305D are located in a genomic region on chromosome 224112 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA), P501S was located on chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification

Isolated polypeptide comprising at least an immunogenic portion of prostate-specific protein, useful in the diagnosis and therapy of

Claim 3; Page 167-168; 325pp; English.

progtate cancer

Harlocker SL, Jiang Y, , Day CH, Skeiky YAW,

Xu J, Dillon DC, Mitcham JL, He Kalos MD, Retter MW, Stolk JA,

WPI; 2001-308785/32

(CORI-) CORIXA CORP.

99US-0439313 99US-0443686

12-NOV-1999; 18-NOV-1999;

09-NOV-2000; 2000WO-US30904

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Pred. No., 0;
; Mismatches
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100.0%; Pr
tive 0;
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hes 553; Conserv
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Human, prostate cancer, therapy, diagnosis, cat eye syndrome, chromosome 22q11.2, prostate-specific protein, chromosome 1, prostate specific antigen, PSA.

Homo sapiens

Human prostate-specific amino acid sequence L1-12/P501S

X8XXXXXXXXXXXXXXXXXXXXXX

(first entry)

553 AA

AAG99002 standard; Protein;

AAG99002;

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181 IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 157-158; 276pp; English.
                                                                                                                                                                                                                                                                                                          AAB74800 standard; Protein; 553 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes compositions comprising peptides derived from the Wilm's tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a polypeptide described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLALLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCRQAYSVYAFMISLGGCLGYLLPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                               Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene; chromosome 11p13; zinc finger transcription factor.
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                                                                                                                                                                                                                                                                                                                                                                                                  Peptide comprising part of the Wilm's Tumour gene product sequence i
1 in the diagnosis and treatment of malignant diseases e.g. leukemia
cancer associated with WII.
RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                              AAG62150 standard; Protein; 553 AA
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                                        VVFDKSDLAKYSA 553
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Best Local Similarity 100.
Matches 553; Conservative
                                                          VVFDKSDLAKYSA
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                                                                                                                                                          301 YQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA
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                                                                                                            YQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA
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241 CCPCRARLAFRNLGALLPRIHOLCCRMPRILRRLFVAELCSWMALMTFTLFYTDFVGGGL
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prostate cancer; immunogenic; cytostatic; vaccine.
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ABG76665 standard; Protein; 553 AA.
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09-FEB-1998;
                     25-FEB-1998;
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                                                                                                                   Xu J,
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                                                                                                                                                                             1 MVORLWVSRLLRHRKAOLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIG
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                                                                                                 553;
   AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are used in the exemplification of the present invention.
                                                                                                   Length
                                                                                                                                         Indels
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                                                                                               Query Match
100.0%; Score 553; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 553; Conservative 0; Mismatches
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01-AUG-1997;
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61 PVLGLVCVPLLGSASDHWRGRYGRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDPRPL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new polypeptide comprising an immunogenic portion of a prostate protein. The invention is useful for inhibiting the development of prostate cancer in a partient. The invention is also useful as markers for diagnoshing prostate cancer for monitoring diseases progression in patients. The present amino acid sequence represents a human prostate tumour protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                     Novel polypeptides useful as vaccines for inhibiting prostate cancer development, comprise an immunogenic portion of prostate protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 553;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 553; DB 23; Best Local Similarity 100.0%; Pred. No. 0; Matches 553; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 59-61; 101pp; English
98US-0020956.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma.
                         RVVPGRGI CLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ
                                                                                                                                                                                                                                                                      481 RVVPGRGICLDLAILDSAFLLSQVAPSLFWGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ
                                                                               AFPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG
                                                                                                      AFPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHEKQVFLPKYRGDTGG
                                                                                                                                                                ASSEDSLMTSFLPGPKPGAPPPNGHVGAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acids that are differentially expressed in mass cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human mast cell related splice variant protein MC14 SEQ ID NO 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB77575 standard; Protein; 553
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2001US-275479P.
2001US-279115P.
2001US-280143P.
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28-MAR-2001;
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ABB77575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contacting a biological sample from a patient with: (a) a binding agent that binds, to a polypeptide having an immunogenic portion of a prostate protein or its variant; (b) 2 oligonuclectide primers, where 1 of the oligonuclectides is specific for a DNA encoding the polypeptide of (a); or (c) an oligonuclectide probe specific for a DNA molecule encoding the polypeptide of (a). The method and polypeptides are useful for polypeptide of (a). The method and polypeptides are useful for progression, and inhibiting the development of prostate cancer in a patient. The polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. ABG76663-ABG76669 represent human prostate tumour protein sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting prostate cancer comprises contacting a sample with an agent capable of binding to a polypeptide with an immunogenic portion of a prostate protein, oligonucleotide primers or a probe specific for DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVQRLWVSRLLRHRKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of detecting prostate cancer by
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                                                                                                                   Human; prostate tumour; immunotherapy; prostate cancer.
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                                                                                                                                                                                                                                                                                                                          97US-0806596.
97US-0904809.
98US-0020747.
                                                                                                                                                                                                                                                                                     98US-0030606
                                                                            Prostate tumour protein #3
                                    (first entry)
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Matches 553; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         553 AA;
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                                    05-NOV-2002
                                                                                                                                                         Homo sapiens
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09-FEB-1998;
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for presenting information to identify the relative expression level of (1). (11) is used as a marker to detect, diagnose or identify an allergic response in a partient. The protein can also serve as a target that modulate gene expression or activity and as an antigen to raise polychonal or monoclonal antibodies. (11) is useful for identifying agents that modulate expression of the protein or agents, such as agonists or antagonists are useful for modulating biological activity and function of (11) and thus are useful for alleviating disease conditions such as allergic hypersensitivity, seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
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ive 0; Mismatches 0; Indels 0;
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cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polymucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polymucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various

present invention relates to methods of detecting a prostate

Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes

are expressed in a prostate tissue Claim 27; Page 386; 436pp; English

Hevezi P;

Afar D,

Wilson KE,

KC,

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2002-471335/50. Mack DH,

N-PSDB; ABK92217

(EOSB-) EOS BIOTECHNOLOGY INC.

24-APR-2001; 2001US-286214P. 30-APR-2001; 2001US-0847046. 04-MAY-2001; 2001US-288589P.

16-MAR-2001; 2001US-276888P. 06-APR-2001; 2001US-281922P. 24-APR-2001; 2001US-286214P.

2000US-0733742. 2001US-263957P.

24-JAN-2001; 16-MAR-2001; 08-DEC-2000; 08-DEC-2000; 13-OCT-2000;

2000US-0733288

2001US-276791P

2001WO-US32045

12-OCT-2001;

18-APR-2002

organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer as a security in the contract of prostate cancer.

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Matches 553; Conservative
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cancer; prostate tumour tissue; human; mammal; cytostatic.

Prostate cancer-associated protein #101.

BXSXXXXXXXXXXXX

Prostate

Mammalia

WO200230268-A2

(first entry)

15-AUG-2002

ABG61900

ABG61900 standard; Protein; 553 AA

RESULT 14 ABG61900

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61 PVLGLVCVPLLGSASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDPRPL 120
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diseases, in particular prostate cancer, and as markers for the
progression of cancer
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100.0%; Score 553; DB 23;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 553; Conservative 0; Mismatches 0;
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gene therapy.
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DILLON D C.
MITCHAM J L.
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Search completed: December 3, 2003, 17:23:03 Job time: 49 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

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2856.916 Million cell updates/sec

US-09-593-793A-113 Title: Perfect score:

553 1 MVQRLMVSRLLRHRKAQLJL......AIYFATQVVFDKSDLAKYSA 553 Seguence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

684280 segs, 185983659 residues Searched:

Total number of hits satisfying chosen parameters: 0 Word size :

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Published Applications AA: Database :

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			Description	Sequence 101, App	Sequence 2, Appli	Sequence 113, App	113,	Sequence 113, App	Sequence 113, App	113,	Seguence 113, App	Sequence 113, App	Sequence 113, App	Sequence 113, App	Sequence 13, Appl	113,	113,	Sequence 113, App
SUMMARIES			ID	US-09-745-288-101	US-09-838-785-2	·US-09-759-143-113	US-09-780-669-113	US-09-030-606-113	US-09-822-827-113	US-09-115-453-113	US-09-232-880-113	US-09-895-793-113	US-09-895-814-113	US-10-144-678A-113	US-10-005-907-13	US-10-294-025-113	US-10-012-896-113	US-10-010-940-113
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61 PVLGLVCVPLLGSASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDPRPL 120

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181 IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH 240

Sequence 947, App Sequence 947, App Sequence 974, App Sequence 974, App Sequence 974, App Sequence 1029, Ap Sequence 1029, Ap Sequence 708, App Sequence 708, App Sequence 708, App Sequence 708, App Sequence 852, App Sequence 1028, App Sequence 1028, App Sequence 1028, App Sequence 1028, App Sequence 1021, App Sequence 1021, App Sequence 1011, Ap	AND AND AND AND AND AND AND AND	Length 553; Indels 0; Gaps 0; PLLIEVGVEEKEMTMVLGIG 60
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181 IDWDTSALAPYLGTQBECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH 240
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION WHERE: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
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ive 0; Mismatches
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Patent No. US20020022248A1
GENERAL INFORMATION:
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Vedvick, Thomas S
Carter, Darrick
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Matches 553; Conservative
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ORGANISM: Homo sapien
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SEQ ID NO 113
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100.0%; Score 553; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 553; Conservative 0; Mismatches
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PRIOR FILING BATE: 2000-04-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver: 2.0
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US-09-838-785-2
Sequence 2, Application US/09838785
Patent No. US2002009455A1
GENERAL INFORMATION:
APPLICANT: Lau; Ted
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Parry, Gordon
Schneider, Douglas
Steinbrecher, Renate
Van Heuit, Pam T
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ORGANISM: Homo Bapiens
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LENGTH: 553
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                                                              IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH
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APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
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Patent No. US20020051977A1
GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Panger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Skeiky, Yasir A.W.
Hepler, William
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US-09-780-669-113'
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Length 553;

DB 9;

100.0%; Score 553;

Query Match

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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FC
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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                                                                                1 MVQRLWVSRLLRHRKAQLLLVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKPMTMVLGIG
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Pred. No. 0;
0; Mismatches
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 113, Application US/09030606
Patent No. US20020081580A1
100.08;
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                   553; Conservative
Best Local Similarity
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US-09-030-606-113
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Best Local Similarity 100.
Matches 553; Conservative
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapien
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US-09-115-453-113
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US-09-115-453-113
                                                US-09-822-827-113
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FITLE REFERENCE: 210121.5341.
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
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100.0%; Score 553; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 553; Conservative 0; Mismatches
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Patent No. US20020081680A1
GENERAL INFORMATION:
                TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
    TELECOMMUNICATION INFORMATION
                                                                           LENGTH: 553 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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US-09-030-606-113
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US-09-822-827-113
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Patent No. US20020090372A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SSOTHARE: FaetSEQ for Windows Version 3.0
SSOTHARE: FaetSEQ for Windows Version 3.0
SSOTHARE: 533
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Query Match
100.0%; Score 553; D
Best Local Similarity 100.0%; Pred. No.,0;
Matches 553; Conservative 0; Mismatches
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                                                            181 IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210.121.5.34C.2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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Skeiky, Yasir A.W.
Hepler, William T.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
Li, Samuel X.
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ORGANISM: Homo sapien
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US-09-895-793-113
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APPLICANT: Xlllon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880
CURRENT FILING DATE: 1999-01-15
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100.0%; Score 553; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 553; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
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; Publication No. US20020182596A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapien
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US-09-232-880-113
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Best Local Similarity 100.
Matches 553; Conservative
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ORGANISM: Homo sapien
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                                Length 553;
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100.0%; Score 553; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 553; Conservative 0; Mismatches
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Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
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Publication No. US20020193296A1
GENERAL INFORMATION:
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Skeiky, Yasir A.W.
Hepler, William T.
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                       FOR THE THERAPY
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: OOMFOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0 |
SEQ ID NO 113
LENGTH: 553
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Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Renderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
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RESULT 13
US-10-294-025-113
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIACROSIS OF PROSIATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION UMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
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Skeiky, Yasir A. W.
Hepler, William T.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
Watanabe, Yoshihiro
             Day, Craig H.
Vedvick, Thomas
Carter, Darrick
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Stolk, John A.
                                                     Li, Samuel X.
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APPLICANT: Union Chimique Belge, S.A.
APPLICANT: Union Chimique Belge, S.A.
APPLICANT: No. US20030166881Alka, Karl
APPLICANT: Pirozzi, Gregory
APPLICANT: Einstein, Richard
TITLE OF INVENTION: ACTIVATION
FITLE OF INVENTION: ACTIVATION
FILE REFERENCE: 0535.9-5005
CURRENT APPLICATION NUMBER: US/10/005,907
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
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; EBERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
Sequence 13, Application US/10005907
Publication No. US20030166881A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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301 YQGVPRAEPGTEARRHYDEGVRMGSLGLFLYQCAISLVFSLVMDRLVQRFGTRAVYLASVA 360
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APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/10/12,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SEQ ID NO 113
LENGTH: 553
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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                                                                                                                                                            Henderson, Robert
  Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
Li, Samuel X.
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Matches 553; Conservative
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CORGANISM: Homo sapiens
US-10-012-896-113
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APPLICANT: Stolk, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER FILE REFERENCE: 210121.427029
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT APPLICATION NUMBER: US/10/294,025
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSEQ for Windows Version 3.0
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; Publication No. US20020183251A1
; GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
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ORGANISM: Homo sapiens
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US-10-012-896-113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 YQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 ASSEDSIMISFIPGPKPGAPFPNGHVGAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 ASSEDSLMTSFLPGPKPGAPFPNGHVCAGGSGLLPPPPALCGASACDVSVRVVVGEPTEA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVQRLWVSRLLRHRKAQLLLVNLLFGLEVCLAAGITYVPPLLLEVGVEEKFMTMVLGIG 60
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                           ; PRUBLICATION NO. USZUGJOUBBUGZALI
; FURDILGAMTION NO. USZUGJOUBBUGZALI
; APPLICAMT: Dillon, Davin C.
; APPLICAMT: Mitcham, Jennifer L.
; APPLICAMT: Ralos, Michael
; APPLICAMT: Reter, Mark
; APPLICAMT: Reter, Mark
; APPLICAMT: Reter, Mark
; APPLICAMT: Bolk, John
; TITLE OF INVENTION: UNAGER: US/10/010,940
; TITLE OF INVENTION: UNAGER: US/10/010,940
; FILE REFERENCE: 210121.42703
; CURRENT APPLICATION NUMBER: US/10/12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15; Length 553;
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100.0%; Score 553; Dest Local Similarity 100.0%; Pred. No. 0; Matches 553; Conservative 0; Mismatches
; Sequence 113, Application US/10010940
; Publication No. US20030088062A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WFDKSDLAKYSA 553
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Search completed: December 3, 2003, 17:25:48 Job time: 37 secs

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version	- 2003
GenCore	(c),1993
	Copyright

OM protein - protein search, using sw model

December 3, 2003, 17:20:47; Search time 40 Seconds (without alignments) 3567:577 Million cell updates/sec Run on:

US-09-593-793A-113

553 1 MVQRLWVSRLLRHRKAQLLL......AIYFATQVVFDKSDLAKYSA Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

830525 seqs, 258052604 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

0

Word size : ·

830525

Post-processing: Listing first 45 summaries

sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_bacteriap:* sp_organelle:*sp_phage:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* rvirus:* SPIREMBL 23:* sp_fungi:*
sp_human:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

		Description	Q96jt2 homo sapien	Q95ki5 macaca fasc	Q95kc5 macaca fasc	Q8k252 mus musculu	Q8k0h7 mus musculu	Q8r1i0 mus musculu	Q8nfh8 homo sapien	043428 homo sapien		Q8d101 synechococc	Q9fv92 solanum tub	Q9fvj6 lycopersico	Q8e9z4 shewanella	Q9qjc6 human immun	Q90ua8 human immun	Q93pb7 microscilla
COLUMNICO		ID	Q96JT2	Q95KIS	Q95KC5	Q8K252	Q8K0H7	Q8R110	Q8NFH8	043428	OBNF15	Q8DL01	Q9FV92	Q9FVJ6	Q8E9Z4	920060	Q90UA8	Q93PB7
		四 :	4	φ.	9	11	11	11	4	4	4	16	10	10	16	15	15	7
	* Query	Length	553	553	501	450	553	112	520	521	629	305	488	200	631	68	115	120
	& Query	Match	100.0	28.6	23.7	10.7	10.7	6.0	1.8	1.8	1.8	1.6	1.6	1.6	1.6	1.4	1.4	1.4
		Score	553	158	131	29	59	33	10	10	10	0	δ	6	σ	80	80	Φ.
	Result	No.	7	7	e	4.	S	y	7	80	თ	10	11	12	13	14	15	16

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Q91te6 arabidopsis Q81di6 arabidopsis Q8yVF3 anabaena sp Q94DF3 caronchabdi Q911z3 oryza sativ Q8r8K3 thermoanaer Q8r8K3 thermoanaer Q8r8K9 methanopyru Q9xbn0 rhodococcus Q8dbf6 vibrio vuln Q598G10 fibriobium 1 Q592F7 bacillus sp Q942n6 oryza sativ Q942n1 arabidopsis Q942n1 streptomyce Q942n1 streptomyce Q942n1 carbidopsis Q9mr4 arabidopsis Q9mr4 arabidopsis Q9mr4 arabidopsis Q9mr4 citrus sine	TS 3 AA. ce update) tion update) tion update) vertebrata; Buteleon i; Hominidae; Homo. J., Zhang X., Hought: S.G.; prostein, a novel prostein, a novel prostein, a novel prostein, and prostein.	100.0%; Score 553; DB 4; Length 553; similarity 100.0%; Pred. No. 0; s, Conservative 0, Mismatche 0; Indels 0; Gaps 0; MVORLWYSRLIRHRKAQLILVNLLTFGLEVCLAAGITYVPPLLLEVGVEEKFWITWLGIG 60
091T86 081V89 094075 094075 094075 081XX9 081XY9 095X80 095X80 095X80 095X80 095X80 095X80 005448 095X81 005529 095X81 095X81 095X81 095X81	ALIGNMENTS VARY; PRT; 553 rel. 19, Created) rel. 19, Last sequence rel. 19, Last annotati Chordata; Craniata; V Primates; Catarrhini; DMed=11245466; N., Badaro R., Reed S characterization of p 11568 (2001). 4386.1; OAFA23FBC7	Score 553; Pred. No. 0; Mismatches NLLTFGLEVCLA
	. Cr 9, Ca 9, La 111245, 111245, A. Zadaro cteri 2001)	0%; 0%; 0LLLV
1135 1135 1146 1176 1176 1176 1176 1176 1176 1176		100.0%; 100.0%; vative LLRHRKAQLI LLRHRKAQLI
**************************************	T 1 2 296JT2 PRELIMINARY 096JT2 01-DEC-2001 (TEMBLEEL) 01-DEC-2001	Similarity 100 Similarity 100 3; Conservative MVORLWVSRLIRHRK
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1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 Q96JT2 ID Q96JT2 DT 01-DEC-2001 (TrEM) DT 01-DEC-2001 (TrEM) DT 01-DEC-2001 (TrEM) DE PROSTEIN OS HOMO SAPIGNS (Hum) OC MAMMALIA; Butheri, OX NCEL SEQUENCE FROM N.A RP SEQUENCE FROM N.A RY TISSUE-PROSTATE; RX MEDLINE-21139994; RX MEDLINE-21139994; RA Filho AM., Nolas RT "Identification and RT "Identification and RT SEQUENCE RES. 61:15 RESULVE PROSTATE RY MEDLINE-21139994; RA Filho AM., Nolas RT "Identification and RT Seculation AND SECULATION	Query Match Best Local Matches 55: Oy 1 Db 1

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422 SSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPALCGASACDVSVRVVVGEPTEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 VVPGRGICLDLAILDSAFILLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQV
                                                                                                                                                                                                                                                                                        TISSUB=Medulla oblongata;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 53.4 kDa protein.
Hypothetical 53.4 kDa protein.
Hypothetical 53.4 kDa protein.
Hypothetical 53.5 kDa protein.
Hypothetical 53.6 kDa protein.
Hypothetical 53.7 kDa protein.
Hadcaca fassicularis (Crab eating macaque) (Cynomolgus monkey).
Hypothetical Mondata; Craniata, Wertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhin; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                           libraries.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB062977; BAB60745.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 501 AA; 53447 MW; 8C554BBD04EE0470 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-07T-2002 (TrEMBLrel. 22, Created)
01-07T-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.7%; Score 131; DB 6; Le
100.0%; Pred. No. | 7.6e-118;
tive 0; Mismatches 0;
                     501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                           Cercopithecinae; Macaca.
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542 VFDKSDLAKYS 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 VFDKSDLAKYS 500
                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2210413P12RIK.
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Matches
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095KC5
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                                             IDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGPTEPAEGLSAPSLSPH 240
                                                                                                                                                                                                             ASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPPALCGASACDVSVRVVVGEPTEA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                               RVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQ 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQGVPRAEPGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRFGTRAVYLASVA 360
                                                                                                                                                                                                                                                                        AFPVAAGATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDTGG 420
                                                                                                                                                                                                                                                                                                 AFPVAAGGATCLSHSVAVVTASAALTGFTFSALOILPYTLASLYHREKOVFLPKYRGDTGG 420
                                                                                                                                                                                                                                                                                                                                                            ASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPPALCGASACDVSVRVVVGEPTEA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VPLLGSASDHWRGRYGRRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDPRPLELALLIL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 VPLLGSASDHWRGRYGRRPFIWALSLGILLSLFLIPRAGWLAGLLCPDPRPLELALLIL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GVGLLDFCGQVCFTPLEALLSDLFRDPDHCRQAYSVYAFMISLGGCLGYLLPAIDWDTSA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCPCRARLAFRNLGALLPRIHQLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGEGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Temporal cortex;
Sada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao Suzuki Y., Sugano S., Habhimoto K.;
Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypotherical 59-4 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.6%; Score 158; DB 6; Length 553; Best Local Similarity 100.0%; Pred. No. 5.8e-144; Matches 158; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB060851; BAB46871.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 553 AA; 59392 MW; 0718F3A91FB3BF1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAPYLGTQEECLFGLLTLIFLTCVAATLLVAEEAALGP 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 AA
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01-DEC-2001
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Q95KI5

RESULT Q95KIS

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Length 501;

481 429 541 489

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159 OLCCRMPRILRRLFVAELCSWMALMTFILFYTDFVGEGLYQGVPRAEPGTEARRHYDEG
                                                                                                                                                                                          262 QLCCRMPRTLRRLFVAELCSWMALMTFTLFYTDFVGEGLYQGVPRAEPGTEARRHYDEG
                                                               Length 450;
450 AA; 48261 MW; 72C703AEC131302C CRC64;
                                                           10.7%; Score 59; DB 11; I
100.0%; Pred. No. 3.8e-48;
ive 0; Mismatches 0;
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16

OBKOH7 RESULT 5 Q8K0H7

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SEQUENCE FROM N.A.
MEDLINE-98066250; PubMed=9422736;
MEDLINE-98066250; PubMed=9422736;
MEDLINE-98066250; Debmed=9422736;
Treda M., Ishida O., Hinoi T., Kishida S., Kikuchi A.;
Treda M., Ishida O., Hinoi T., Kishida S., Kikuchi A.;
Treda M., Ishida and characterization of a novel protein interacting with Ral-binding protein 1, a putative effector protein of Ral.";
J. Biol. Chem. 273-814-821(1998).
BMBL, APO10233; AAC02901.;
InterPro; IPR002048; EF-hand.
InterPro; IPR002046; EPS15_homology.
                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Oosterhoff J.K., Penninkhof F., Brinkmann A.O., Grootegoed A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blok L.J.;
"Role of REPS2/POB1 in progression of prostate cancer.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF512951, AAM43953.1;
InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EPS15_homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57773 MW; C5B4F557D58A444D CRC64;
                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) RALERI associated Eps domain containing protein 2b.
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Last annotation update)
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44 GRGICLDLAILDSAFLLSQVAPSLFMGSIVQLS
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PROSITE; PS50031; EH; 1.
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PROSITE; PS50031; EH; 1.
SEQUENCE 521 AA; 57901 MW;
                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2003 (TrEMBLrel. 23,
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SMART; SM00027; EH; 1.
                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00027; EH; 1.
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043428;
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                                                                                                  RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.0%; Score 33; DB 11; Length 112; Best Local Similarity 100.0%; Pred. No. 1.7e-23; Matches 33; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Straubberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024519; AAH24519.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005805; Rieske.
PROSITE; PS00200; RIESKE_2; 1.
Hypothetical protein.
SEQUENCE 553 AA; 59742 MW; 6A474FEA630B4B13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 AA; 11393 MW; B9D9DE79FEF09FB7 CRC64;
                                                                                                                                          (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 11.4 kba protein (Fragment)
Mus musculus (Mouse)
                                                                                                  553 AA.
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01-MAR-2003 (TrEMBLrel. 23, Last annotati
Hypothetical protein (PROSTEIN homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Urinary bladder;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC031381; AAH31381.1; -.
EMBL; AK035428; BAC29063.1; -.
MGD; MGI:1922082; 2210413P12Rik.
                                                                                                PRELIMINARY;
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Query Match

Matches

Q8R110 O8R110;

RESULT 6 QBR110

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Length 520;

Gaps ó 1.8%; Score 10; DB 4; Length 521; 100.0%; Pred. No. 1.3; 57901 MW; F5FCF51B56961026 CRC64; 100.0%; Pred. No. 1.3 tive 0; Mismatches Query Match 1.85
Best Local Similarity 100.(
Matches 10; Conservative

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485 GRGICLDLAILDSAFLLSQVAPSLFMGSIVQLS 517

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Gaps

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"A new subfamily of sucrose transporters, SUT4, with low Affinity/High capacity localized in enucleate sieve elements of plants."; Plant Cell 12:1345-1356(2000).
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-20407148; PubMed-10948254;
Weise A., Barker L., Kuehn C., Lalonde S., Buschmann H., Frommer W.B.,
                                                                                                                                                                                                                             Sucrose transporter SU14 (Fragment).
Solanum tuberosum (Potato).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
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488 AA; 52840 MW; 0800388914ADAF77 CRC64;
                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
0; Mismatches
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TIGRFAMs; TIGR01301; GPH_sucrose; 1.
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100.0%; Pre
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel; 23,
9; Conservative
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                                                            107 VAAGATCLS 115
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                               364 VAAGATCLS 372
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Les 9; Conserv
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Matches
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Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Complete genome structure of the thermophilic cyanobacterium
                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                       Oosterhoff J.K., Penninkhof F., Brinkmann A.O., Grootegoed A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 10; DB 4; Length 659;
100.0%; Pred. No. 1.5;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                   Blok L.J.;
"Role of REPS2/POB1 in progression of prostate cancer.";
Submitred (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF51153; AAM4933.1; -.
Genew; HGNC:9963; REPS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         527A658BDFB4582B CRC64;
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                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) MAR-2003 (Separated Eps domain containing protein 2a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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100.0%; Pred. No. 7.3;
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TRPC OR TLL0698.
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Interpro; IPR000261; EPS15 homology.
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                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS50031; EH; 2.
                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
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SMART; SM00027; EH; 1.
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                                                                                                                                   PRELIMINARY;
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                 SGLLPPPPAL 460
                                      370 SGLLPPPPAL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 SGLLPPPPAL 460
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                                                                                                                                                                                                                                                    Homo sapiens (Human)
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Best Local Similarity
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01-MAR-2003
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                   451
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                                                                                                                                   Q8NFI5
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QBDL01
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Q8NFI5
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"A new subfamily of sucrose transporters, SUT4, with low affinity/high capacity localized in enucleate sieve elements of plants.";
Plant Cell 12:1345-1355(2000)
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AF176950; AAG09270.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Moneymaker;
MEDLINE=20407148; PubMed=10948254;
Weise A., Barker L., Kuhn C., Lalonde S., Buschmann H., Frommer W.B.,
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum (Tomato). Bubryophyta; Embryophyta; Tracheophyta; Bubrayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Solanales; Solanaceae; Solanum.
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Score 9; DB 10; Length 488;
Pred. No. 11;
0; Mismatches 0; Indels
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Last annotation update)
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          MEDLINE=20170331; PubMed=10708058;
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AIDS; Coat protein; Glycoprotein.
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Pfam; PF00516; GP120; 1.
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Best Local Similarity 100.
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MEDLINE=22297686; PubMed=12368813;

Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,

Read T.D., Elsen J.A., Seahadri R., Ward N., Methe B., Clayton R.A.,

Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,

DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

Wadupu R., Peterson J.D., Umayam M., Lee K., Wolf A.M.,

Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,

Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,

Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;

Shewanella oneidensis."
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Alteromonadaceae; Shewanella.
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                                                                                                                                                                                                                         1.6%; Score 9; DB 10; Length 500; 100.0%; Pred. No. 11; tive 0; Mismatches 0; Indels
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                                                                                                                                                                500 AA; 54274 MW; BFDFAE7468D40110 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
MSHA biogenesis protein MshH.
MSHH OR SO4116.
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Last annotation update)
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100.0%; Pred. No. 14;
tive 0; Mismatches
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005989; Suc/H_symport.
Pfam; PF00083; sugar_tr; 1.
TIGRPAMS; TIGR01301; GPH_sucrose; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015843; AAN57089.1; -.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
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Best Local Similarity 100...
9; Conservative
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LLILGVGLL 138
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                                                                                                                                     Transmembrane.
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QRE924

ID QRE924

OG ORE922

AC QRE922

AC O1-MP

DT 01-MP

DT 01-MP

DT 01-MP

DT 01-MP

DT 01-MP

CO NSHH

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Human immunodeficiency virus 1. Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11676;

SEQUENCE FROM N.A. STRAIN=151N;

Envelope protein (Fragment).

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Casado C., Urtasun I., Martin-Walther M.V., Garcia S., Rodriguez C., del Romero J., Lopez-Galindez C.; "Genetic analysis of HIV-1 samples from Spain."; J. Acquir. Immune Defic. Syndr. 23:68-74(2000)].
EMBL, AF152836; AAF08474.1.-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gunthard H.F., Havlir D.V., Fiscus S., Zhang Z.-Q., Eron J., Mellors J., Gulick R., Frost S.D., Leigh Brown, A.J., Schleif W., Valentine F., Jonas L., Melbohm A., Ignacio C.C., Isaace R., Gamagami R., Emini E., Haase A., Richman D.D., Wong J.K.; "Residual human immunodeficiency virus (HIV) type 1 RNA and DNA in Jymph nodes and HIV RNA in genital secretions and in cerebrospinal fluid after suppression of viremia for 2 years;"; EMBL, AF337292; AAKS6214.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                1.4%; Score 8; DB 15; Length 68;
100.0%; Pred. No. 18;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                        68 68 68 7538 MW; 76B0F5F1734650C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 AA.
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OM protein - protein search, using sw model

Run on:

December 3, 2003, 17:21:22 ; Search time 21 Seconds (without alignments) 2532.442 Million cell updates/sec

US-09-593-793A-113 553 1 MVQRLWVSRLLRHRKAQLLL......AIYFATQVVFDKSDLAKYSA 553 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283308 segs, 96168682 residues Searched:

0 Word size :

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	orobable cation tr			hypothetical prote	hypothetical prote	~~	rRNA (adenine-N6-)	IS1380 polypeptide	endo-1,4-beta-xyla	hypothetical prote	unknown protein F9	phosphotransferase	phosphotransferase	hypothetical prote	probable polynucle	sucrose-proton tra	probable sucrose-p	succinate dehydrog	ActA protein - Lis	IactA protein - Li	nestin - golden ha		hypothetical prote	ŭ	9	al pro	_	gp64 protein - Myc	hetical pr
Ø	E87243	C70752	S16222	AE2058	T25087	JX0222	JS0635	A48971	851779	G87522	C96769	WQEBST	S62331	A86234	D70600	T14339	G84441	E87686	S47245	T43164	T34518	AD3215	A71471	G46449	CCSG6	E87453	T49358	G72807	874529
DB		10	~	~	~	~	-	2		ď	~	_	~	N.			N	N	Ċ	N		ca Ca	C)	Ñ	_		~		
Length [1609	1632	137	142	176	223	260	328	354	.412	445	455	456	474	480	501	594	965	787	1080	1804	68	83	87	89	102	122	128	130
* Query Match	1.6	1.6	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.3	1.3	•	1.3	1.3	1.3	1.3	1.3
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Result No.	-	10	М	4	ß	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25		27	28	29

thymic shared anti	Ξ	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	conserved hypothet		Ξ.		_	hypothetical prote	hypothetical prote	pupI protein - Pse	probable arok prot
149013	C83768	E70845	B65061	B91085	D85930	AF0127	AF0861	S45108	A96493	H83160	S29280	S77324	F70481	846355	G70658
136 2	141 2	146 2	149 1	149 2	149 2	149 2	149 2	151 1	151 2	154 2	155 2	160 2	173 2	173 2	176 2
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7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 E87243 E000bble cation transport ATPase ML2671 [imported] Mycobacterium leprae
	C.brectes: Mycobacterium reprae C.bate: 20-Apr-2001 #Bequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C.brossion: R81243
	<pre>P. Tr. Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M. Nature 409, 1007-1011, 2001</pre>
	A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sqn A; Title: Massive gene decay in the leprosy bacillus. A; Reference number: A86909; MUID:21128732; PMID:11234002
	A; Scression: E87243 A; Scratus: preliminary A; Molecule type: DNA A; Residues: 1-1609 cSTO>
•	A;Cross-references: GB:AL450380; NID:g13093871; PIDN:CAC32203.1; GSPDB:GN00147 C;Genetics: A;Gene: ML2671
	Query Match 1.6%; Score 9; DB 2; Length 1609; Best Local Similarity 100.0%; Pred. No. 8.6; Antches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Oy 17 OLLLVNLLT 25
	THEN CHANGE
	RESULT 2 C70752 probable ctp! protein - Mycobacterium tuberculosis (strain H37RV)
	C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C:Accesion: C70752
	Ricold S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S., Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
	Nature 393, 537-544, 1998 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & Aprile: Decipher, 270500, WITH, 0205037, DMTH, 0204030
, , ,	A. Accession: C70752 A. Status: preliminary; nucleic acid sequence not shown; translation not shown A. Molecule type: DNA
	A;Residues: 1-1632 <col/> A;Cross-references: GB:Z74410; GB:AL123456; NID:g3261600; PIDN:CAA98940.1; PID:e1299890; A;Experimental source: strain H37Rv
	C;Genetics: A;Gene: ctpI C;Superfamily: ATPase nucleotide-binding domain homology

Page

us-09-593-793a-113.rpr

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ubiquitin thiolesterase (EC 3.1.2.15) PGP9.5 - rat
N.Alternate names: ubiquitin carboxy-terminal esterase; ubiquitin carboxyl-terminal hydro
C.Species: Rattus norvegicus (Norway rat)
C.Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 10-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: JX0222
R;Kajimoto, Y.; Hashimoto, T.; Shirai, Y.; Nishino, N.; Kuno, T.; Tanaka, C.
A. Biochem. 112, 28-32, 1992
A;Title: cDNA cloning and tissue distribution of a rat ubiquitin carboxyl-terminal hydroll
A;Reference number: JX0222; MUID:93054416; PMID:1331034
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Gene 108, 55-62, 1991
A;Title: Cloning and characterization of two genes from Streptomyces lividans that confer
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                                                                                                                                                                                                                                                                                                                  C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T25087
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C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Introns: 25/1; 83/1; 112/1
C;Superfamily: Caenorhabditis elegans hypothetical protein T21H8.5
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                                                                                                                                                                                                                                                                                                  elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, August 1996
A;Reference number: Z19979
A;Accession: T25087
A;Status: preliminary; translated from GB/EMBL/DDBJ
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1.4%; Score 8; DB 2;
Best Local Similarity 100.0%; Pred. No. | 13;
Matches 8; Conservative 0; Mismatches
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1.4%; Score 8; |DB 2
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                  lypothetical protein T21H8.5 - Caenorhabditis
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A;Experimental source: brain
C;Superfamily: human ubiquitin thiolesterase
C;Keywords: thiolester hydrolase
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                               97 LLSLFLIP 104
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                                                                                                           93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-176 <WIL>
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                                                                                                           86 LLSLFLIP
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AB2058
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C;Species: Bombina variegata (yellow-bellied toad)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jul-2000
C;Accession: S1622; A44581
R;Simmaco, M.; Barra, D.; Chiarini, F.; Noviello, L.; Melchiorri, P.; Kreil, G.; Richter Eur. J. Blochem. 199, 217-222, 1991
A;Title: A family of bombinin-related peptides from the skin of Bombina variegata.
A;Reference number: S16222; MUID:91293126; PMID:1712299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-137 <SIM>
A; Residues: 1-137 <SIM>
A; Cross-references: GB:X59695; NID:g62568; PIDN:CAA42216.1; PID:g62569
A; Cross-references: GB:X59695; NID:g62568; PIDN:CAA42216.1; PID:g62569
R; Mignogna, G:, Simmaco, M; Kreil, G.; Barra, D.
EMBO J. 12, 4829-4832, 1993
A; Title: Antibacterial and haemolytic peptides containing D-alloisoleucine from the skin A; Reference number: S39612; MUID:94038967; PMID:8223491
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F;111-136/Product: bombinin H #stetus experimental <MAT>
F;118/Modified site: D-allo-isoleucine (11e) (in mature form) #status experimental
F;118/Modified site: amidated carboxyl end (11e) (amide in mature form from following
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7;1237-1406/Domain: ATPase nucleotide-binding domain homology <ATN>
                                                                           Length 1632;
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                                                                   1.6%; Score 9; DB 2;
100.0%; Pred. No. 8.7;
rative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches
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100.0%; Pred. No. 11;
ive 0; Mismatches
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C;Genetics:
A;Gene: alr2019
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A,Residues: 117-136 <MIG>
C,Superfamily: bombinin H precursor
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                       Local Similarity 100
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A; Residues: 1-142 < K
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                                                                           Query Match
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Matches
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Cispecies: Caulobacter crescenting
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Cispeciesion) (8
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dacesion: C96769
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C96769
                                                                                                                                                              G; Function:
A; Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A; Description: degradation
A; Pathway: xylan degradation
C; Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase bomology
C; Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
C; Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
C; Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F; R:1-27/Pomain: signal sequence #status predicted <WAT>
F; B-354/Product: endo-1,4-beta-xylanase homology <XIL>
F; B-223/Domain: endo-1,4-beta-xylanase homology <XIL>
F; B-20,210/Active site: Glu #status predicted
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A;Cross-references: GB:AE005673; NID:g13423711; PIDN:AAK24179.1; GSPDB:GN00148
C;Genetics:
TTG for residue 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appothetical protein CC2208 [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 354;
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    the authors translated the initiation codon
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100.0%; Pred. No. 23;
ative 0; Mismatches
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100.0%; Pred. No. 27;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Residues: 1-445 <STO>
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                                                                                   A;Gene: xynY
A;Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: CC2208
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                              A,Accession: JS0635
A;Molecule type: DNA
A;Residues: 1-260 <JEN>
A;Residues: 1-260 <JEN>
A;Cross-references: GBN74717; NID:g153345; PIDN:AAA26779.1; PID:g153346
A;Experimental source: strain TK21
C;Comment: This enzyme confers resistance to lincomycin.
C;Comment: This enzyme catalyzes the monomethylation of a specific adenosine within 23S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.15.18 polypeptide homolog - Bradyrhizobium japonicum
C; Species: Bradyrhizobium japonicum
C; Species: Bradyrhizobium japonicum
C; Species: 19-Dec-1933 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C; Accession: 448971
R; Judd, A.K.; Sadowsky, M.J.
Appl. Environ. Microbiol. 59, 1656-1661, 1993
Appl. Environ. Microbiol. 59, 1656-1661, 1993
A; Title: The Bradyrhizobium japonicum serocluster 123 hyperreiterated DNA region, HRS1, A; Reference number: 448971; MUID: 93298005; PMID: 8390818
A; Reference number: nucleic acid
A; Status: preliminary
A; Molecule type: nucleic acid
A; Residuse: 1-328 «JUD»
A; Experimental source: USDA 424
A; Note: sequence extracted from NCBI backbone (NCBIN: 133925, NCBIP: 133926)
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A, Residues: 1-354 < HYU>
A, Cross-references: EMBL.X59059; NID:g487722; PIDN:CAA41784.1; PID:g1334251
A, Experimental source: strain YA-335
B, Ju-Hyun, Y.; Park, Y.S.; Yum, D.Y.; Kim, J.M.; Kong, I.S.; Bai, D.H.
M. And Tottechnol. 3, 139-145, 1993
A, Title: Nucleotide sequence and analysis of a xylanase gene (xyns) from alkali-tolerant A, Reference number: S48126
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551779
600-1,4-beta-xylanase (EC 3.2.1.8) Y precursor - Bacillus sp. (strain YA-33
N'Alternate names: xylanase Y
C;Species: Bacillus sp.
A;Variety: strain YA-335
C;Date: 15-Jul-1995 #sequence_revision 22-Nov-1996 #text_change 16-Jun-2000
R;Hyun Ju, Y.
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A; Reference number: JS0635; MUID:92104506; PMID:1761231
                                                                                                                                                                                                                                                                                                                                                                        A.Gene: lrm
C.Superfamily: rRNA (adenine-N6-)-methyltransferase
C.Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8; DB 1;
Pred. No. 18;
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100.0%; Pred. No.
0; Mismatches
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submitted to the EMBL Data Library, December 1990
A;Reference number: S51779
A;Accession: S51779
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-17,19-229 <-UUH>
A;Cross-references: EMBL:X59059
A;Experimental source: strain YA-335
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Best Local Similarity 100.
Matches 8; Conservative
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-802, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
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C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: 070600
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
                                                                                                          A Molecule type: DNA

A. Residues: 1-456 < RIT.

A. Residues: 1-456 < RIT.

A. Scross-references: EMBL.X57401; NID:943931; PIDN:CAA40658.1; PID:943933

R. Schmid, K.; Ebner, R.; Jahreis, K.; Lengeler, J.W.; Titgemeyer, F.

R. Schmid, K.; Ebner, R.; Jahreis, K.; Lengeler, J.W.; Titgemeyer, F.

A. Title: A sugar-specific porin, Scry, is involved in sucrose uptake in enteric bacteria A; Reference number: S15193; MUID:91312133; PMID:1649946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X57401; NID:g43931; PIDN:CAA40658.1; PID:g43933
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-474 <STO>
A;Cross-references: GB:AE005172; NID:g2160188; PIDN:AAB60751.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: scrA
C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor
C;Keywords: membrane protein; phosphotransferase; sugar transport system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein [imported] - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S15195
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-456 <SCH>
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sucrose-6-phosphate invertase.
A,Reference number: S62329; MUID:96188840; PMID:8628219
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Pred. No. 29;
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100.0%; Pred. No. 30;
tive 0; Mismatches
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1.4%; Score s; ub & Best Local Similarity 100.0%; Pred. No. 29; Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                               A, Accession: S62331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphotransferase system enzyme II (EC 2.7.1.69), sucrose-specific, factor II - Salmone NyAlternate names: phosphotransferase system enzyme II-sucrose; protein-Npi-phosphohisti C; Species Salmonella typhimurium C;Date: 31-Mar-1991 #text_change II<sup>L</sup>Jun-1999 (C;Accession: S01036; S62329; $35016 (R;Ebner, R; Lengeler, J.W. Mol. Microbiol. 2, 9-17, 1988 (A;Tile: DNA sequence of the gene scrA encoding the sucrose transport protein enzyme-II(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ם
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C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor II
C;Keywords: membrane protein; phosphoprotein; phosphotransferase; sugar transport system
F;308/Active site: His #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;MOJECTILE TYPE: DNA
A;Residues: 1-7,9-24,'HC',26-36,38-46,49-76,78-140,'N','A',145-207,'E',211-230,'V','EKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jahreis, K.; Lengeler, J.W.
Ol. Microbiol. 9, 195-209, 1993
Ol. Microbiol. 9, 195-209, 1993
Filtle: Molecular analysis of two ScrR repressors and of a ScrR-FruR hybrid repressor; Reference number: S35014; MUID:94018607; PMID:8412665
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C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 18-Jun-1999
C;Accession: S62331; S15195
R;Titgemeyer, F; Jahreis, K; Ebner, R.; Lengeler, J.W.
Mol. Gen. Genet. 250, 197-206, 1996
A;Title: Molecular analysis of the scrA and scrB genes from Klebsiella pneumoniae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Y00541; NID:g47925; PIDN:CAA68605.1; PID:g47926
R;Titgemeyer, F; Jahreis, K.; Ebner, R.; Lengeler, J.W.
R01. Gen. Genet. 250, 197-206; 1996
A;Title: Molecular analysis of the scrA and scrB genes from Klebsiella pneumoniae and
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A;Readidues: 1-24, 'HCC', 26-435,'IAFGVARTV', 445-455 <JAH>
A;Cross-references: EMBL:X67750; NID:G395262; PIDN:CAA47973.1; PID:G395263
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
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       A;Cross-references: GB:AE005173; NID:g10092422; PIDN:AAG12827.1; GSPDB:GN00141
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                                                                                                                                                                                     Length 445;
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A;Accession: $01036
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A,Reference number: S62329; MUID:9618840; PMID:8628219
                                                                                                                                                                                         DB 2;
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1.4%; Score 8; DB 2,
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches
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                                     C,Genetics:
A,Gene: F9E11.3
A,Map position: 1
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A.Authors. Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors. Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295897; PMID:9634230
A;Retus: preliminary, nucleic acid sequence not shown; translation not shown A;Residues: 1-480 <COL>
A;Experimental source: strain H37Rv
C;Genetics:
A;Genetics:
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Query Match

1.4%; Score 8; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 254 GALLPRIH 261 ò

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Search completed: December 3, 2003, 17:24:59 Job time: 22 secs

375 GALLPRLH 382

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OM protein - protein search, using sw model

Run on:

December 3, 2003, 17:19:51; Search time 18 Seconds (without alignments) 1444.765 Million cell updates/sec

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553 1 MVQRLWVSRLLRHRKAQLLL......AIYFATQVVFDKSDLAKYSA 553 Title: Perfect score:

Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

127863 seqs, 47026705 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

SwissProt_41:* Database :

Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Reg

	Description	O53114 mycobacteri	Q10900 mycobacteri		_	P29006 bombina var	P82286 bombina var												P83083 bombina max	033603 streptococc	Q46917 escherichia		Q47418 erwinia car		P95014 mycobacteri	P16032 mesembryant	P38477 marchantia	P44201 haemophilus	_			6		Q9vna4 drosophila
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	COLJ ONCMY	YCBR_BACSU	HMD1_CHICK	6PGL_HUMAN	MRAY THEMA	EBP2 HUMAN	EBP2 MOUSE	YNH2 CABEL	NU1M_SQUAC	RFBC NEIGO	OSTY YEAST	PUR6_METTH	
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	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

		ycetales;	nomson N.R., arris D., Connor R.,	Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jaggls K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Sajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,	phate. Jein. ATPases family (P-type	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	EMBL; AL022118; CAA17934 1; - EMBL; AL583926; CAC32203.1; - PIR; E80243; E87243. EPIR; E80243; E87243. InterPro; IPR001057; ATPase_E1-E2. InterPro; IPR001059; HATPase. InterPro; IPR001052; HATPase; 1. PEAN; PF00122; E1-E2 ATPase; 1. PRINTS; PR00119; CATATPASE. PRINTS; PR00119; CATATPASE. PRINTS; PR00119; ATPASE. PROSTITE; PS00154; ATPASE E1 E2; 1. COMPLETE PROTECTION; Magnesium; ATP-binding;
	—e	tinom erium.	C., H.	Macle Macle Macle Macle Macle Macle Macle	osphat cotein t ATP	uced to and are no its collage picture.	unesian
1609 AA.	update) n update) I (EC 3.6.3	eridae; Ac Mycobacte	, James K. Churcher 11:noworth	eltwell T. acroix C., jandream M onds M., S	sive gene decay in the leprosy bacillus."; re 409:1007-1011(2001). CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the cation transport ATPas ATPases).	It is produ If is produ Hong as i emoved. Us t (See http	5. ation, Mag
PRT;	Created) Last sequence update) Last annotation update) Octing ATPase I (EC 3.6	02. Actinobact eriaceae;	.234002; trkhill J. trnier T.,	hoy S., F fels K., L M.A., Ra 1 S., Simm	leprosy b + H(2)O integral m the catio	copyright. tute of Bioi ics Institut titutions as ent is not r nse agreemen nse@isb-sib.	E1-E2. Be. Be. Be. Be. '; 1. '; 1. '; 1. '; 1. '; 1. '; 1.
STANDARD;	40, Created) 40, Last sec 42, Last and ansporting A	MLCB1913. rae. cteria; A Mycobact	PubMed=11 er K., Pa ore N., Ga	n K., Dut yy T., Jag K., Quail K., Simon IS K., Tay	y in the (11 (2001). VITY: ATP (CATION: I longs to	OT entry is col- Swiss Institute Bioinformatics profit institu- this statement ires a license ail to license	1022118; CAA17934 1; 1583926; CAC32203.1; 1543; E87243; E87243. 1512671;
STA	(Rel. (Rel. (Rel.	71 OR m lepr tinoba ineae;	M N.A. 18732; iglmei	Devli Hornsk Niver Geeger Steven	ie deca 007-10 C ACTI LAR LO TY: Be	ROT en Swiss Swiss Bioin Profi Lthis Unires	2118; CAA.1 3926; CAC.3 3926; CAC.3 12,61; 112,7; 112,001,7; 12,000,000,000,000,000,000,000,000,000,0
RESULT 1 CTPI MYCLE ID CTPI MYCLE	USJ114; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence un 15-SEP-2003 (Rel. 42, Last annotation Probable cation-transporting ATPase I	CTPI OR ML2671 OR MLCB1913.02. Mycobacterium leprae. Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. NCBI_TaxID=1769;	[1]	Davies R.M., Holroyd S., Murphy L., C Rutter S., S Squares S.,	Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001)	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinform the Buropean Bioinformatics Institute. Use by non-profit institutions as lon modified and this statement is not removentities requires a license agreement (Sont send an email to license@isb-sib.ch).	EMBL; ALO22118; CAA17934 1; EMBL; AL583926; CAC32203.1; - PIK; B8742; B8743; E8743. Interpro; IPR001757; ATPase_E1-E2. Interpro; IPR001757; ATPase_E1-E2. Interpro; IPR00159; H ATPase. Pfam; PP00122; E1-E2 ATPase; I- Pfam; PP00122; B1-E2 ATPase; I- PRINTS; PR00119; CATATPASE. TIGRFAMS; TIGR01494; ATPase P-type; PROSITE; P800154; ATPASE. COMPLESE; Transmembrane; Phosphoryl Complete proteome.
RESULT CTPI M	864448	88888	8 8 8 8 8 8 8 8 8	2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3	888888888	388888888	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. |There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
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Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
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MDBLINE=2403867;
Mignogna G., Simmaco M., Kreil G., Barra D.;
MARIDACterial and haemolytic peptides containing D-alloisoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
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1625 AA; 167805 MW; 54082AD7064C22EB CRC64;
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15-SEP-2003 (Rel. 42, Last annotation update)
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InterPro; IPR001757; ATPase_B1-E2.
InterPro; IPR001695; H_ATPase.
InterPro; IPR005834; Hydrolase.
Pfam; PF00122; B1-E2_ATPase; I.
Pfam; PF00702; Hydrolase; I.
PRINTS; PR00119; CATATPASE.
TIGRFAM8; TIGR01494; ATPASE_B1 E2; I.
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30-MAY-2000 (Rel. 39, Last seq
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EMBL; AE006923; AAK44338.1;
PIR; C70752; C70752.
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                                                                                                                                                                                                                                                               rigr; MT0116; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY; ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Geeger K., Skelton S., Squares B.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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POTENTIAL.

PHOSPHORYLATION (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

166871. MW; 58FA2079905E3995 CRC64;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI TaxID=1773,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1609;
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16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable cation-transporting ATPBASE I (EC 3.6.3.-).
CTPI OR RV0107C OR MI0116 OR MTCY251.26C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
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Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mignoria Co., Simmaco M., Kateli G., Barra D.;

"Antibacterial and haemolytic peptides containing D-alloisoleucine
"Antibacterial and haemolytic peptides containing D-alloisoleucine
from the skin of Bombina variegata.";

EMBO J. 12:4829-4831(1993).

-!- FUNCTION: HAS ANTIMICROBIAL ACTIVITY, BUT NO HEMOLYTIC ACTIVITY.

--- FUNCTION: BOMBININ H HAS ANTIBACTERIAL AND HEMOLYTIC ACTIVITY.

--- SUNCTION: BOMBININ H HAS ANTIBACTERIAL AND HEMOLYTIC ACTIVITY.

--- SUNCTION: SPECIFICITY: Skin.

--- SIMILARITY: BELONGS TO THE BOMBININ PAMILY.
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dasic residues; Signal; Hemolysis; D-amino acid.

18 POTENTIAL.

43 ACIDIC PEPTIDE 1-1 (POTENTIAL).

70 BOMBININ-LIKE PEPTIDE 1.
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                                                                                                                                                SEQUENCE FROM N.A., AND PRELIMINARY SEQUENCE OF 44-69.
TISSUB-Skin, and Skin secretion;
MEDLINE-91293126; PubMed=1712299;
Simmaco M., Barra D., Chiarini F., Noviello L., Melchiorri P.,
Kreil G., Richter K.;
"A family of bombinin-related peptides from the skin of Bombina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCTAPEPTIDE (POTENTIAL).
ACIDIC PEPTIDE 1-2 (POTENTIAL).
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Pfam; PF05298; Bombinin; 1.
Amphibian defense peptide; Antibiotic; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 199:217-222(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94038967; PubMed=8223491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Skin secretion;
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                                                         Amphibia; Batrach
NCBI_TaxID=8348;
                                                                                                                                                                                                                                                                                                                                                    variegata."
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                    DE DIT DIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bombina variegata (Yellow-bellied toad).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Bombinin-like peptides 1 precursor (Contains: Acidic peptide 1-1;
Bombinin-like peptide 1 (BLP-1); Octapeptide 1; Acidic peptide 1-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skin secretion;
MEDLINE=94038967; PubMed=8223491;
Mignogna G., Simmaco M., Kreil G., Barra D.;
"Antibacterial and haemolytic peptides containing D-alloisoleucine
                                                                                                                                                                                                                                                                                                        D-ALLO-ISOLEUCINE.
AMIDATION (G-21 PROVIDE AMIDE GROUP)
08C7281E1D6D43BD CRC64;
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AMIDATION (G-21 PROVIDE AMIDE GROUP)
08C7281E1BDBF3BD CRC64;
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0
                                                                                                                                      -i- TISSUE SPECIFICITY: Skin.
-i- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
Amphibian defense peptide; Antibiotic; Hemolysis; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: Skin.
-!- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
Amphibian defense peptide; Antibiotic; Hemolysis; Amidation;
D-amino acid.
                                                  EMBO J. 12:4829-4832(1993).
-!- FUNCTION: HAS ANTIMICROBIAL AND HEMOLYTIC ACTIVITIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, AND POST-TRANSLATIONAL MODIFICATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOH5_BOMVA STANDARD; PRT; 21 AA. P82285; 30-MAY-2000 (Rel. 39, Last sequence update) 15-SFP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 AA
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                                                                                                                                                                                                                                                                                BOMBININ H4
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from the skin of Bombina variegata.";
EMBO J. 12:4829-4812/1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the skin of Bombina variegata.";
EMBO J. 12:4829-4832(1993).
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                                                                                                               SUBCELLULAR LOCATION: Secreted.
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2 2
20 20
21 AA; 1975 MW;
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21 AA; 1975 MW;
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IGPVLGLV 9
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                                                                                                                                                                                                                                           D-amino acid.
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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BOH5_BOMVA
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BLP1_BOMVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAWATAN Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
Azawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Azawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Rhotel P., Lewis S., Matsuo Y., Nikaido I., Fesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suvuki R., Tomita M., Magner L., Mashio T.,
RA Bake J., Boffelli D., Bojunga N., Carninci P., de Bonado M.F.,
RA Brownstein M.J. Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,
Sasaki H., Sato K., Schoenbach C., Seyal T., Shibata Y., Storch K.-F.,
Whithaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Andriachizaki Y.
                                                                                                             Saigoh K., Wang Y. L., Suh J.G., Yamanishi T., Sakai Y., Kiyosawa H., Harada T., Ichihara N., Wakana S., Kikuchi T., Wada K.; "Intragenic deletion in the gene encoding ubiquitin carboxy-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).

-!- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS. THIS ENTER BY A THIOL PROTEINS. THAT RECOGNIZE AND HYDROLYZE A PEPTIDE BOND AT THE C.TERMINAL GLYCINE OF UBIQUITIN.
-!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2) 0 = ubiquitin + a thiol.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J, TISSUB=Pituitary; Marzban G., Grillari V., Reisinger B., Hemetsberger T., Hohenwarter O., Katinger H.; "Cloning of the mouse homologue of ubiquitin carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- TISSUE SPECIFICITY: Expressed in brain and testis.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001578; UCH 1.
Pfam; PF01088; Peptidase_C12; 1.
PRINTS; PR00707; UBCTHYDRLASE.
Probom; P0350662; UCH 1; 1.
UBL conjugation pathway; Hydrolase; Thiol 3
ACT_SITE 90 90 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6J; TISSUE-Hippocampus;
MEDLINE-21085660; Pubmed=11217851;
                                                                        TISSUE=Brain;
MEDLINE=99400551; PubMed=10471497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB025313; BAA84083.1; -.
EMBL, AP172334; AAD51029.1; -.
EMBL, AK013729; BAB28976.1; -.
                                                                                                                                                                                           hydrolase in gad mice.";
Nat. Genet. 23:47-51(1999).
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                         hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 117-136.
TISSUB=Skin, and Skin secretion;
MEDILNE=99566278; PubMed=1033736;
Simmaco M., Mignogna G., Barra D.;
"Antimicrobial peptides from amphibian skin: what do they tell us?";
Biopolymers 47:435-450(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                           TISSUE=Skin secretion;
MEDLINE=94038967; PubMed=8223491;
Mignogna G., Simmaco M., Kreil G., Barra D.;
"Antibacterial and haemolytic peptides containing D-alloisoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION (G-71 PROVIDE AMIDE GROUP).
AMIDATION (G-137 PROVIDE AMIDE GROUP)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UBL1 MOUSE STANDARD, PRT, 223 AA.

QBR0F9, QBR122;

16-OCT-2001 (Rel. 40, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UL) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5) UCHL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCTAPEPTIDE (POTENTIAL).
ACIDIC PEPTIDE 2-2 (POTENTIAL).
BOMBININ H2.
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                                                                                                                                                                                                                                                                                     SEQUENCE OF 117-136, AND POST-TRANSLATIONAL MODIFICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibian defense peptide; Antibiotic; Amidation;
Cleavage on pair of basic residues; Signal; Hemolysis.
SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4%; Score 8; DB 1;
100.0%; Pred. No. 4.7;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          from the skin of Bombina variegata.";
EMBO J. 12:4829-4832(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15035 MW;
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                                                                   NCBI_TaxID=8348;
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SEQUENCE
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protease; Multigene family.

BY SIMILARITY

MOUSE

Matches

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Best Local Similarity
                  Matches
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                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thiol protease; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS. THIS ENZYME IS A THIOL PROTEASE THAT RECOGNIZES AND HYDROLYZES A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN. CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "cDNA cloning and tissue distribution of a rat ubiquitin carboxyl-
                                                                                                                                                                                                                                                                       000981;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
02-FEB-2003 (Rel. 41, Last annotation update)
Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (IL1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminal hydrolase PGP9.5.";
J. Biochem. 112:28-32(1992).
-!- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
                                                                                                                                 ö
                              UBIQUITIN BINDING 1 (POTENTIAL) UBIQUITIN BINDING 2 (POTENTIAL)
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UBIQUITIN BINDING 2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93054416; PubMed=1331034;
Kajimoto Y., Hashimoto T., Shirai Y., Nishino N., Kuno T.,
Tanaka C.;
                                                                                                 1.4%; Score 8; DB 1; Length 223; 100.0%; Pred. No. 7; 0; Indels tive 0; Mismatches 0; Indels
                                                                      F1402BF7B0C077EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F1BA04FB55B4625E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ubiquitin + a thiol.
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
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 BY SIMILARITY
BY SIMILARITY
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178 UB
24782 MW;
                                                                      24838 MW;
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                                                                                                                               Conservative
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                         420 GASSEDSL 427
                                                                                                                                                                                     GASSEDSL 193
                                                                      223 AA;
                                                                                                               Local Similarity
Les 8; Conserv
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ACT_SITE
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                                        DOMAIN
CONFLICT
SEQUENCE
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SEQUENCE
                                                                                                   Query Match
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UBL1_RAT
ID UBL1_F
                                                                                                                            Matches
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Length 223;

DB 1;

1.4%; Score 8;

Query Match

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Titgemeyer F., Jahreis K., Ebner R., Lengeler J.W.;

"Molecular analysis of the scrA and scrB genes from Klebsiella
molecular analysis of the scrA and scrB genes from Klebsiella
Titgemeyer F., Jahreis K., Ebner R., Lengeler J.W.;

"Molecular analysis of the phosphotransferase system and a
sucrose-6-phosphate invertase.";

"Molecular Enzyme II Scr of the phosphotransferase system and a
sucrose-6-phosphate invertase.";

Molecular Enzyme II Scr of the phosphotransferase system and a
sucrose-6-phosphate invertase.";

Molecular Enzyme II Scr of the phosphotransferase system and a
sucrose-6-phosphate invertase.";

Molecular Engyme II Scr Off 1996).

"The Strand This Is A COMPONENT OF THE PHOSPHORNOLD-YRUVATE-DEPENDENT
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL, THE IIA DOWALN CONTAIN THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO
THE SUGAR. EIIBC-SCR BELONGS TO THE BIIBC DOMAIN TYPE AND LACKS A
COVALENTLY BOUND EIID DOMAIN. INSTEAD, EII-SCR-MEDIATED
COVALENTLY BOUND SITE MAJOR GLUCOSE TRANSPORT SYSTEM.

CIC, A COMPONENT OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

CIC, A COMPONENT OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

CIC, A COMPONENT OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

INSTEAD OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

CIC, A COMPONENT OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

INSTEAD OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

CIC, A COMPONENT OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

INSTEAD OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.

CIC, SIMILARITY: Contains 1 PTS EIIG domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PTS system, sucrose-specific IIBC component (BIIBC-SCR) (Sucrose-permase IIBC component) (Phosphotransferase enzyme II, BC component)
(EC 2.7.1.69) (BII-SCR).
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphotransferase system; Transport; Sugar transport; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales:
Enterobacteriaceae; Klebsiella.
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                          Indels
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                     0; Mismatches
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Pfam; PF02378; PTS EIIC; 1.
TIGRPAMB; TIGR00826; EIIB_glc; 1.
TIGRPAMB; TIGR00852; pts-Glc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=1033-5P14 / KAY2026;
MEDLINE=96188840; Pubmed=8628219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
InterPro; IPR004719; PTSIIC_glc.
100.08;
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                       8; Conservative
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132
164
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                                                                  420 GASSEDSL
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J. Bacteriol. 173:449-456(1991).
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "DNA sequence of the gene scrA encoding the sucrose transport protein EnzymeII(Scr) of the phosphorransferase system from enteric bacteria: homology of the EnzymeII(Scr) and EnzymeII(Sgl) proteins."; MOI. Microbiol. 2:9-17(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1988 (Rel. 08, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
PTS system, cucrose-specific IIBC component (EIIBC-SCR) (Sucrose-permage IIBC component) (Phosphotransferase enzyme II, BC component)
(EC 2.7.1.69) (EII-SCR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Titgemeyer F., Jahreis K., Ebner R., Lengeler J.W.; "Molecular analysis of the scrA and scrB genes from Klebsiella penemoniae and plasmid purkto, which encode the sucrose transport protein Enzyme II Scr of the phosphotransferase system and a sucrose-6-phosphate invertase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                            PHOSPHORYLATION (BY SIMILARITY). |
PHOSPHORYLATION (BY SIMILARITY). |
4AFDF5405CAEFC66 CRC64;
                                                                                                                                                                                                                                           Length 456;
                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=88216186; Pubmed=3285123;
Ebner R., Lengeler J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
REVISIONS.
MEDLINE=94018607; PubMed=8412665;
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MEDLINE=91100329; PubMed=1846143;
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                                                                                                                                                                                                                                                                                     8; Conservative
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267
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408
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Best Local Similarity
                                                                                                                                                                                                     456 AA;
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P08470;
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SUGAR PHOSPHOTRANSPERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS (CONTAIN THE SUGAR BINDING SITE AND THE TRANSFEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT PO THE SUGAR. EIIBC-CRR BELONGS TO THE BILD DOMAIN TYPE AND LACKS A COVALENTLY BOUND EIIA DOMAIN. INSTEAD, EII-SCR-MEDIATES IT CORPOSHORYLATION OF SUCROSE REQUIRES, THE ACTIVITY OF ENZYME IIA-GLC, A COMPONENT OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

CATALITIC FOR STATISM OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

CATALITIC FORDING OF SUCROSE REQUIRES, THE ACTIVITY OF ENZYME IIA-GLATIC ACTIVITY. Protein N-phosphohistidine + sugar phosphate.

SUBSELLULAR LOCATION: Integral membrane protein. Inner membrane.
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PROSITE; PSO1035; PTS_EIIB_CYS; 1.
PROSITE; PSO1035; PTS_EIIB_CYS; 1.
Plosphotransferase system; Transferase; Phosphorylation.
DOMAIN 112 456 EIIC DOMAIN.
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AC 054697;
AC 054697;
AC 054697;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41)
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-!- SIMILARITY: Contains 1 PTS EIIC Gomain.
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001996; PTS EIIB.
InterPro; IPR003352; PTS EIIC.
InterPro; IPR00419; PTSIIC_glc.
Pfam; PP00367; PTS EIIB; 1.
ProDom; PP00318; PTS EIIB; 1.
TIGRFAMS; TIGR00826; EIIB glc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y00541; CAA68605.1; ALT_SEO.
EMBL; X67750; CAA47973.1; -.
EMBL; M38416; AAA98418.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47864 MW;
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Best Local Similarity
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497

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490 LDLAILDS
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                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma. COFACTOR: Zinc; Binds two ions per subunit (By similarity). SUBCELULIAR LOCATION: Type II membrane protein. Ileal brush border
                                                                                                     STRAIN-Sprague-Davley; TISSUE-Ileum;
MEDLINE-98049571; PubMed=9388249;
Shneider B.L., Thevananther S., Moyer M.S., Walters H.C., Rinaldo P.,
Devarajan P., Sun A.Q., Dawson P.A., Ananthanarayanan M.;
"Cloning and characterization of a novel peptidase from rat and human ileum.";
J. Biol. Chem. 272:31006-31015(1997).
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-ALA.
NUCLEOPHILE (NAALADASE) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02225; PA; 1.
Pfam; PF04389; Peptidase_M28; 1.
Pfam; PF04353; TFR dimer; 1.
Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Aminopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                Biol. Chem. 272:31006-31015(1997).
FUNCTION: Has no NAAG hydrolyzing activity (By similarity).
EXHIDIS a dipeptidyl-peptidase IV type activity. In vitro, cleaves Gly-Pro-AmC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 1 (POTENTIAL).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
N-LINKED (GLCNAC. ...) (POTENTIAL N-LINKED (GLCNAC. ...) (POTENTIAL N-LINKED (GLCNAC. ...)
                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Mainly expressed in the distal small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dipeptidase, Serine protease, Transmembrane, Glycoprotein, Sgral-anchor; Multifunctional enzyme.

CytOpLaSMIC (POTENTIAL).

TRANSMEM 7 28 SIGNAL-ANCHOR (TYPE-II MEMBRA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8; DB 1;
Pred. No. 19;
0; Mismatches
                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 4-17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF009921; AAB87644.1; -.
MEROPS; M28.011; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80640 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               745 AA;
                                                            NCBI_TaxID=10116;
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383
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SEQUENCE
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 4:215-230(1997).
-!- FUNCTION: INVOLVED IN TRANSPORT OF PHOSPHOLIPIDS.
-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSTIE; PS00114; ATPASE E1_E2; 1.
Hydrolage; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                        Gomes E., Jakobsen M.K., Axelsen K.B., Geisler M., Palmgren M.G.; "Chilling tolerance in Arabidopsis involves ALA1, a member of a new family of putative aminophospholipid translocases."; Plant Cell 12:2441-2454(2000).
                                                                                                                                                                     (Aminophospholipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Columbia;
BEDLINE-2741969; PubMed=9330910;
Sato S., Kotani H., Nakamura Y., Kaneko T., Agamizu E., Fukami M.,
Miyajima N., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
EXTRACELLULAR (POTENTIAL)
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                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Phospholipid-transporting ATPase 1 (EC 3.6.3.1)
                                                                                    PRT; 1158 AA
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InterPro; IPR005834; Hydrolase.
Pfam; PF00702; Hydrolase; 1.
TIGRPAMs; TIGR01652; ATPase-Plipid; 1.
TIGRRAMs; TIGR01494; ATPASE P-type; 7.
PROSITE; PS00154; ATPASE E1_E2; 1.
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EMBL; AB005245; BAB11515.1; -.
InterPro; IPR001757; ATPase_E1-E2.
                                                                                                                                                                                                      OR AT5G04930 OR MUG13.22.
                                                                                    STANDARD;
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PubMed=11148289;
 LDLAILDS
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                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clones.";
                                                                                    ARATH
                                                                                                                                                                                      flippase 1
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TRANSMEM
DOMAIN
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Rhodobacteraceae; Paracoccus.
       NCBI_TaxID=187400;
                             SEQUENCE FROM N.A
                                        STRAIN=R114;
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P00118;
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CYC6 SPIMA
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                                                                                                                                                                                      Gaps
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Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
NCBI TaxID=161274;
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Skin secretion;
Chen T.B., McClean S., Orr D.F., Bjourson A.J., Rao P.F., Shaw C.;
"Isolation and structural characterisation of antimicrobial peptides
from the venom of the Chinese large-webbed bell toad (Bombina
                                                                                                                                                                                                                                                                                                                                           Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paracoccus zeaxanthinifaciens.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
                                                                                                           PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MW; SCC042B40C8C94D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable exodeoxyribonuclease VII small subunit (EC 3.1.11.6)
                                                                                                                                                                 DB 1; Length 1158;
                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 20;
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EXTRACELLULAR (POTENTIAL)
                                       EXTRACELLULAR (POTENTIAL)
                                                                               EXTRACELLULAR (POTENTIAL)
                   CYTOPLASMIC (POTENTIAL).
                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EC7541AA1BF3BD49 CRC64;
                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     maxima).";
Submitted (JUL-2001) to the SWISS-PROT data bank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: Has antimicrobial activity.
-i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUB SPECIFICITY: Skin.
-i- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.
Amphabian defense peptide; Antibiotic.
SEQUENCE 20 AA; 1947 MW; EC7541AA1BF3BD49 C.
                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 AA.
                                                                                                                                                                           28;
                                                                                                                                                                      100.0%; Preu. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.3%; Score 7; DB 1
100.0%; Pred. No. 9.1
:ive 0; Mismatches
                                                                                                                                                       1.4%; Score 8; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exonuclease VII small subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                          Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                STANDARD;
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                                                                               1090
1115
1158
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                                                                                                                                  863 86
1158 AA;
                                                                                                                                                                                                          96 ILLSLFLI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GPVLGLV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPVLGLV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EX7S PARZE
Q8L1H9;
                                                                                                                                                                                                                                                                                 BOMMX
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MOD_RES
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EX7S PARZE
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DT 15-SE
DT 15-SE
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GN XSEB.
OG BACKE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. | There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch);
                                                                                                                            -1- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity).
-1- CATALYTIC ACTYVITY: Exonucleolytic cleavage in either 5'- to 3'- or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
-1- SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome C6 (Soluble cytochrome f) (Cytochrome c553) (Cytochrome c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ambler R.P., Bartsch R.G.;
"Amino acid sequence similarity between cytochrome f from a blue-green bacterium and algal chloroplasts.";
Nature 253:285-288(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sawaya M.R., Krogmann D.W., Serag A., Ho K.K., Yeates T.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Structures of cytochrome c-549 and cytochrome c6 from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                               Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 78;
                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8492 MW; 1D3963A65D5C53D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spirulina maxima (Arthrospira maxima).
Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
NCBI_TaxID=1155;
Huembelin M.; "Genetics of isoprenoid biosynthesis in Paracoccus zeaxanthinifaciens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h similarity 100.0%; Pred. No. 28; 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
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Biochemistry 40:9215-9225(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP, MF 00337; -; 1.
InterPro; IPR0376; Exonuc VII_S.
Taran; Pr05269; Exonuc VII_S; 1.
TIGREAMS; TIGR01280; xseB; 1.
Hydrolage; Nuclease; Exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21371781; PubMed=11478889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ431697; CAD24424.1; -.
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21-JUL-1986 (Rel. 01, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kerfeld C.A.;
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Kerfeld C.A., Sawaya M.R., Krogmann D.W., Yeates T.O.;
"Structure of cytochrome of from Arthrospira maxima: an assembly of 24 subunits in a mearly symmetric shell.",
Acta Crystallogr. D.58:1104-1110(2002).
-!- FUNCTION: Functions as an electron carrier between membrane-bound cytochrome bof and photosystem I in oxygenic photosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- FTM: Binds one heme group per molecule.
-!- PTM: Binds one heme group per molecule.
                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the cytochrome c family. PetJ subfamily. PIR; A00110; CCSG.
PDB; 1PIF; 08-AUG-01.
PDB; 1RIB; 03-JUL-02.
HAMAP; MF_00594; -; 1.
InterPro; IPR003088; Cyt_CIC.
InterPro; IPR003045; Cyt_CIC.
InterPro; IPR003045; Cyt_Cic.
PFamily PF00034; Cyt_Cic.
PFamily PF00034; Cyt_Cheme_bind.
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(COVALENT).

(HEME AXIAL LIGAND).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9236 MW; 4796D56B3EA8AF85 CRC64;
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Best Local Similarity 100.
Matches 7; Conservative
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BINDING 14
BINDING 17
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